GenBank Reference

Prior Art. Part of 09/95,85

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: April 6, 2004, 15:41:39 ; Search time 1892 Seconds
(without alignments)
4.134 Million cell updates/sec

DM nucleic - nucleic search, using sw model

Title:
Perfect score: 1476
Sequence: 1 atggcgggcccgagcgctg..........ggcattaactggcaggtga 1476

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.0

Searched: 18 seqs, 2649592 residues
Total number of hits satisfying chosen parameters: 36

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : *txt:*
1: /home/sdavid/sdavid-tmp/apr04/kaufman898/8388586.txt:*
2: /home/sdavid/sdavid-tmp/apr04/kaufman898/8439214.txt:*
3: /home/sdavid/sdavid-tmp/apr04/kaufman898/8518138.txt:*
4: /home/sdavid/sdavid-tmp/apr04/kaufman898/9214222.txt:*
5: /home/sdavid/sdavid-tmp/apr04/kaufman898/9797863.txt:*
6: /home/sdavid/sdavid-tmp/apr04/kaufman898/11024490.txt:*
7: /home/sdavid/sdavid-tmp/apr04/kaufman898/11043617.txt:*
8: /home/sdavid/sdavid-tmp/apr04/kaufman898/11071629.txt:*
9: /home/sdavid/sdavid-tmp/apr04/kaufman898/11071694.txt:*
10: /home/sdavid/sdavid-tmp/apr04/kaufman898/11071692.txt:*
11: /home/sdavid/sdavid-tmp/apr04/kaufman898/13162004.txt:*
12: /home/sdavid/sdavid-tmp/apr04/kaufman898/12273743.txt:*
13: /home/sdavid/sdavid-tmp/apr04/kaufman898/13443401.txt:*
14: /home/sdavid/sdavid-tmp/apr04/kaufman898/13992004.txt:*
15: /home/sdavid/sdavid-tmp/apr04/kaufman898/11723770.txt:*
16: /home/sdavid/sdavid-tmp/apr04/kaufman898/16151411.txt:*
17: /home/sdavid/sdavid-tmp/apr04/kaufman898/16444690.txt:*
18: /home/sdavid/sdavid-tmp/apr04/kaufman898/16444698a.txt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID		Description
c 1	1416	95.9	177822	8	AL358412	ACCESSION:AL358412
c 2	1416	95.9	173352	10	AL358412	ACCESSION:AL358412
c 3	1416	95.9	173761	11	AL358412	ACCESSION:AL358412
c 4	1416	95.9	177798	9	AL358412	ACCESSION:AL358412
c 5	1416	95.9	178044	12	AL358412	ACCESSION:AL358412
c 6	1412.8	95.7	179542	13	AL358412	ACCESSION:AL358412
c 7	1404.8	95.2	179698	16	AL358412	ACCESSION:AL358412
c 8	1404.8	95.2	179700	15	AL358412	ACCESSION:AL358412
c 9	1404.8	95.2	179848	14	AL358412	ACCESSION:AL358412
c 10	1382.2	93.6	170967	7	AL358412	ACCESSION:AL358412
c 11	1132.8	76.7	132164	5	AL358412	ACCESSION:AL358412
c 12	1084.4	73.5	161914	3	AL358412	ACCESSION:AL358412
c 13	1084.4	73.5	161919	4	AL358412	ACCESSION:AL358412
c 14	1084.4	73.5	161919	2	AL358412	ACCESSION:AL358412
c 15	1009.2	68.4	137266	6	AL358412	ACCESSION:AL358412

RESULT 1
AL358412
AL358412/c

LOCUS	AL358412	172822 bp	DNA	linear	HTG	29-OCT-2000

DEFINITION Homo sapiens chromosome 1 clone RP11-509F14, *** SEQUENCING IN
PROGRESS ***, 16 unordered pieces.
ACCESSION AL358412
VERSION AL358412.8 GI:11071629
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 172822)
AUTHORS Sims,S.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT requests: clonerequest@sanger.ac.uk
[WARNING] On Nov 1, 2000 this sequence was replaced by a newer
version gi:11071692.
On Nov 1, 2000 this sequence version replaced gi:11043617.
-------------------- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-------------------- Project Information
Center project name: bA509F14
-------------------- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 166541 bases at least Q40
Consensus quality: 168510 bases at least Q30
Consensus quality: 169709 bases at least Q20
Insert size: 171122; sum-of-contigs
Insert size: 189168; agarose-fp
Quality coverage: 5.07x in Q20 bases; sum-of-contigs Quality
coverage: 4.73x in Q20 bases; agarose-fp
* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

ALIGNMENTS

	No.	Score	%	Length	DB	ID	Description
c	16	749.401	50.8	113959	1	AL358412	ACCESSION:AL358412
c	17	444.398	30.1	113959	1	AL358412	ACCESSION:AL358412
c	18	368.197	24.9	161914	3	AL358412	ACCESSION:AL358412
c	19	368.197	24.9	161914	4	AL358412	ACCESSION:AL358412
c	20	366.597	24.8	137266	6	AL358412	ACCESSION:AL358412
c	21	336.397	22.8	170967	7	AL358412	ACCESSION:AL358412
c	22	189.999	12.9	170967	7	AL358412	ACCESSION:AL358412
c	23	187.399	12.7	178822	8	AL358412	ACCESSION:AL358412
c	24	185.599	12.6	179698	16	AL358412	ACCESSION:AL358412
c	25	184.599	12.5	179700	15	AL358412	ACCESSION:AL358412
c	26	182.599	12.4	179542	13	AL358412	ACCESSION:AL358412
c	27	182.599	12.4	173761	11	AL358412	ACCESSION:AL358412
c	28	182.599	12.4	177798	9	AL358412	ACCESSION:AL358412
c	29	182.399	12.3	179542	13	AL358412	ACCESSION:AL358412
c	30	181	12.3	179542	14	AL358412	ACCESSION:AL358412
c	31	181	12.3	179848	14	AL358412	ACCESSION:AL358412
c	32	167.6	11.4	132164	5	AL358412	ACCESSION:AL358412
c	33	59.202	4.0	9462	17	AL358412	ACCESSION:AL358412
c	34	59.202	4.0	9462	18	AL358412	ACCESSION:AL358412
c	35	45.2001	3.1	9462	17	AL358412	ACCESSION:AL358412
c	36	45.2001	3.1	9462	18	AL358412	ACCESSION:AL358412

```
*  be preserved.

*       1      9825: contig of 9825 bp in length
*    9826      9925: gap of 100 bp
*    9926     26225: contig of 16300 bp in length
*   26226     26325: gap of 100 bp
*   26326     29517: contig of 3192 bp in length
*   29518     29617: gap of 100 bp
*   29618     35632: contig of 6015 bp in length
*   35633     35732: gap of 100 bp
*   35733     52129: contig of 16397 bp in length
*   52130     52229: gap of 100 bp
*   52230     58764: contig of 6535 bp in length
*   58765     58864: gap of 100 bp
*   58865     69646: contig of 10782 bp in length
*   69647     69746: gap of 100 bp
*   69747     81453: contig of 11707 bp in length
*   81454     81553: gap of 100 bp
*   81554     89383: contig of 7830 bp in length
*   89384     89483: gap of 100 bp
*   89484     96472: contig of 6989 bp in length
*   96473     96572: gap of 100 bp
*   96573    110585: contig of 14013 bp in length
*  110586    110685: gap of 100 bp
*  110686    127141: contig of 16456 bp in length
*  127142    127241: gap of 100 bp
*  127242    137550: contig of 10309 bp in length
*  137551    137650: gap of 100 bp
*  137651    150953: contig of 13303 bp in length
*  150954    151053: gap of 100 bp
*  151054    154039: contig of 2986 bp in length
*  154040    154139: gap of 100 bp
*  154140    172822: contig of 18683 bp in length.

FEATURES             Location/Qualifiers
     source          1..172822
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /clone="RP11-509F14"
                     /clone_lib="RPCI-11.2"
     misc_feature    1..9825
                     /note="assembly_fragment:02378
                     fragment_chain:1
                     clone_end:T7
                     vector_side:left"
     misc_feature    9926..26225
                     /note="assembly_fragment:02511
                     fragment_chain:1"
     misc_feature    26326..29517
                     /note="assembly_fragment:01460
                     fragment_chain:1"
     misc_feature    29618..35632
                     /note="assembly_fragment:02024
                     fragment_chain:1"
     misc_feature    35733..52129
                     /note="assembly_fragment:02317
                     fragment_chain:2"
     misc_feature    52230..58764
                     /note="assembly_fragment:02019
                     fragment_chain:2"
     misc_feature    58865..69646
                     /note="assembly_fragment:01132
                     fragment_chain:2"
     misc_feature    69747..81453
                     /note="assembly_fragment:00531
                     fragment_chain:3"
     misc_feature    81554..89383
                     /note="assembly_fragment:01072
                     fragment_chain:3"
     misc_feature    89484..96472
                     /note="assembly_fragment:00103"
     misc_feature    96573..110585
                     /note="assembly_fragment:01228"
     misc_feature    110686..127141
                     /note="assembly_fragment:02552"
     misc_feature    127242..137550
                     /note="assembly_fragment:00061
                     fragment_chain:4"
     misc_feature    137651..150953
                     /note="assembly_fragment:02470
                     fragment_chain:4"
     misc_feature    151054..154039
                     /note="assembly_fragment:00422
                     fragment_chain:4"
     misc_feature    154140..172822
                     /note="assembly_fragment:02480
                     fragment_chain:4
                     clone_end:SP6
                     vector_side:right"

Query Match     95.9%;  Score 1416;  DB 8;  Length 172822;
Best Local Similarity   4.9%;  Pred. No. 2.5e-08;
Matches 1476;  Conservative    0;  Mismatches    0;  Indels 28706;  Gaps    6;

Qy      1 ATGGCGGGGGCCCCGAGCGCGTGGGGGCCCCCTGCTTCCTGTGCCTGCGCTGCGAGGCCGCT------ 54
          ||||||||||||||    ||||||||||||||||||||||||||||||||| ||  |  ||||
Db  34445 ATGGCGGGGGCCCCCAGCGCGTGGGGGCCCCCTGCTTCCTGTGCCTGCTGCGCGCCGCTCCAGGT 34406

Qy     55 ------------------------------------------------------------ 54
Db  34405 AAGGGGCGCGGGGCCCGCGGGAGGGGGAAGAGGGGCTCCCCGGGGCGCGGGCCTAC 34346

Qy     55 ------------------------------------------------------------ 54
Db  34345 CCTCGGACCCGGAGCTCCTGGGACAGGACGCACGGGGGTCCGCAGCCACCGAGCGCGGGGTGCCA 34286

Qy     55 ------------------------------------------------------------ 54
Db  34285 ATCCGGCCCCTGCCTTACGCGCGCCCCCAGTTGCTTCTTCCCAGGACTGAACAGAACCGGGGTCT 34226

Qy     55 ------------------------------------------------------------ 54
Db  34225 TTGATATATTCCTCTTCCCGCAGGAAAACGAAATCAGTTTCCTAARTGCTTCCAGCTTCAGGAGA 34166

Qy     55 ------------------------------------------------------------ 54
Db  34165 ACTGGAGAGAAAAAAAGACAGCGGCGCAGTTTGATACGTGCATATATTTTTAATAAAGTGGCTTTT 34106

Qy     55 ------------------------------------------------------------ 54
Db  34105 ATGTTTCCTAAAAGAAAAGCACACTGATCCCTGCGTGAAAAACCACACTTGACCCTAAAGTGTGG 34046

Qy     55 ------------------------------------------------------------ 54
Db  34045 ACAGCAGGGAAAAGTGGGACCGGATTGATGTCCCTTCCCGTTCCTGCAGGCCTTCTGGTGGG 33986

Qy     55 ------------------------------------------------------------ 54
Db  33985 ACGGAGCTCTGGTCGCCCTGTGCCCTGCTTTCTAACAAGACGGCTTTCTTTTTGGTGGTGGT 33926

Qy     55 ------------------------------------------------------------ 54
Db  33925 TGTTGTTTTGTTGTTTGTTTGTTGTTTGTTGTTTGTTGTTTCCCACCTCTACTGA 33866

Qy     55 ------------------------------------------------------------ 54
Db  33865 TGAGTAAGGTGTCAGGTACAAAAATTCCTCGCCGTAGGACCCAACCACCAAACCTCACCGC 33806

Qy     55 ------------------------------------------------------------ 54
Db  33805 CCACGACTCCAACGAAGCAGGGAAGAAGTCCAGAAATCGCCCCCAGGATATATTTTCC 33746

Qy     55 ------------------------------------------------------------ 54
Db  33745 TAGTCTTTGGACTCACAGTTTAAAGAGCTGTAAAGGTCCCTGGGCATAATCAAATCATCAT 33686
```

```
Qy       55 ------------------------------------------------------------ 54
Db    33685 AAAAGCCTTATATTTATTCAGCAACTTCTTTGTGCCAGGCACCGCATTATTCTGGAAGCCT 33626

Qy       55 ------------------------------------------------------------ 54
Db    33625 CACGACCCAGCCATCCTCGGAGGTAGAGATATTATTTTTACTTTTCCGATGGGAAAACTGAG 33566

Qy       55 ------------------------------------------------------------ 54
Db    33565 GCTCAGAGAGCAATTCAGGGAATTCCTCAAGAAGGATGGGCAGAGAGGTGAGGCACAGAAGAG 33506

Qy       55 ------------------------------------------------------------ 54
Db    33505 AGAAGAGGGGCTAAAGCAAAGCCTGGCTAGCTTTTGCCTCCAGGGTAGGCACGTGGGACAG 33446

Qy       55 ------------------------------------------------------------ 54.
Db    33445 GCTGGTCCATCCACTGGGGTCACTAGGCCAGCCACCAGGGATGCTCCAGCCCCCAGTGCCCACAG 33386

Qy       55 ------------------------------------------------------------ 54
Db    33385 CAGGGTTCTCTGTTGGCTGATGAGGGACCGTGTACCTGTGTGTGGAGGGAGGGTGGGGTCT 33326

Qy       55 ------------------------------------------------------------ 54
Db    33325 TCTGTTCCCCTTTCACTGTCAAACCCAGACCTTCTTGTACTTTCACCTGATTAAGTTATTTA 33266

Qy       55 ------------------------------------------------------------ 54
Db    33265 AATACACAACTAACTATGTGTTGATGATTAGGAGTAAGTACAGCCAGATCTAAGTT 33206

Qy       55 ------------------------------------------------------------ 54
Db    33205 CAAATACTGGCTCCCACACAAACTGACTGTGTTAGCCTCAGGCAGTTAGTTAGCATCTGT 33146

Qy       55 ------------------------------------------------------------ 54
Db    33145 CTCTGAGGCTAGGCGCCCTTTCCATGGAAGCAGAAATGAACTACCCCATAGGGTGG 33086

Qy       55 ------------------------------------------------------------ 54
Db    33085 TCTGTGTCCAAGGGGTGATTGAGGTTTTACATGTAAAGAGGCCAAACTAGTGTGCCATCCT 33026

Qy       55 ------------------------------------------------------------ 54
Db    33025 TTGAAGGCTTCATAGAGGAAAGTTGCTCTAACTGCTGTTTTTCTCATGTGACCTAGCTCG 32966

Qy       55 ------------------------------------------------------------ 54
Db    32965 AATCTGGGGACTGTCCTGCCCATAGGATACCTTACAAGTGCTTGCGAGACAGCCTGGGTCT 32906

Qy       55 ------------------------------------------------------------ 54
Db    32905 CCTGCTCGGTCACCGTTAGGAGGAAGTCAGGAGGTAGTAATAGCACTAGCCTCGTG 32846

Qy       55 ------------------------------------------------------------ 54
Db    32845 GTGATACAGTCCCAGCTTAGAGGACACAGGATGAGGTGGAAGCAGGCACCCCACTTTTGGGT 32786

Qy       55 ------------------------------------------------------------ 54
Db    32785 CTAGAAGGTGATGGGTAGGCAGCCGAGGCTGGGACGCCATCCACAGAACTGGACCCTC 32726

Qy       55 ------------------------------------------------------------ 54
Db    32725 CCTCCCTGATCCATTTGCAAACCCGTATGGCACATGGCACTGGGACACTTCA 32666

Qy       55 ------------------------------------------------------------ 54
Db    32665 GGACCCTGAATTCTCCATGGGACCANGAGCTCCTATAGGGCAGGAATGAAGTGTGTTCT 32606
```

```
Db    32605 TCTTTGAAACCCTGGCACCGTGGTCAACAGATCTTGTTGACTCGTAGTGGTCAATA 32546
Qy       55 ------------------------------------------------------------ 54

Db    32545 GATGGAATAGTTGGAATCATAAAGCTCAATAGACCCCATGAGAGAACCTAGAGAGACAAAGTA 32486
Qy       55 ------------------------------------------------------------ 54

Db    32485 CAGTCAAGAGCTCGGACTTTGGAGTTGGCTAGGCCTGGACTGGAATCTGATTCTACAAACTT 32426
Qy       55 ------------------------------------------------------------ 54

Db    32425 AATAGCTGAGAGAGGGCCCTTGGTTTTCCCATCGTGTAACGGTTATAATTATTAAATGAATAC 32366
Qy       55 ------------------------------------------------------------ 54

Db    32365 CTACCTCCTAGGGATGTTAATGAGGATTAAAAGAGAAAGTGCAGGTAAACTGTTTAGCACA 32306
Qy       55 ------------------------------------------------------------ 54

Db    32305 GAAACCTGGCTCACAGAACACAATACACATTAGCTGCTATTATTATTATTATTTTATT 32246
Qy       55 ------------------------------------------------------------ 54

Db    32245 TATTTATTTTGAGACAGAGTCTCACTCTGTCACCCAGGCCTGGAGTGCGCGCAATCT 32186
Qy       55 ------------------------------------------------------------ 54

Db    32185 CGGCTCACTGCAAACCTCCACCTATCGGGGTTCAAGCAATTCTCGTGTTCTCCCAG 32126
Qy       55 ------------------------------------------------------------ 54

Db    32125 TAGCTGAGATCAGACAGGCGTGTGCCACCATGCCCACTAATTTTGTATTTTAGAAGAGA 32066
Qy       55 ------------------------------------------------------------ 54

Db    32065 CGTGGGTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAGGTGATTTGCCTA 32006
Qy       55 ------------------------------------------------------------ 54

Db    32005 CCTCTGCCTCCCAAAATGTCTGGGATCACAGGGGTGGAGTTACCATGCCCGGCCTTAGCTGC 31946
Qy       55 ------------------------------------------------------------ 54

Db    31945 TATTATTATTCATCATCGTTATCATCATCACCTCGTAGTAGTATGTCAAGGAAGATT 31886
Qy       55 ------------------------------------------------------------ 54

Db    31885 CCCTGGAGGAAGTGACATTTGAATCAAGTATTCAAAGACTAGATGGTGAAATACCAGGCA 31826
Qy       55 ------------------------------------------------------------ 54

Db    31825 GTCAAAGACACCTGGGGTTTAAAAACATCCAGAAGAAATGCAGTCGTGGCTTGGCAACATCGAG 31766
Qy       55 ------------------------------------------------------------ 54

Db    31765 AGGAAGAGATTGCCTGATTGAGCCTGTTGGGGTGGTAGCTGTTGGGAGAGAGCAGCAAGAGAGGCCT 31706
Qy       55 ------------------------------------------------------------ 54

Db    31705 GGCCAGGCGCAGGCCCACGTCAGGCCTGCAGCAGGGCCTCACAAACCTCAATAACAAATGTGGA 31646
Qy       55 ------------------------------------------------------------ 54

Db    31645 CTTTATTCTGAGGCCAAGAGAAAGGGCATGAAACTGGGGAGGAGTTGGTGTAATCAGAGTGCGTAT 31586
Qy       55 ------------------------------------------------------------ 54

Db    31585 TTCAGAAGATTGAAGGATTAACAGTGAGAAAAGTGTGCCACAGAGGGGGAAATAGAGGTCA 31526
Qy       55 ------------------------------------------------------------ 54
```

```
Db 31525 GTTAAAGGGAGGAGTCAGGGAAAGTGTCCTCGAGACAGTGACATCAAAGGAATTGTGAAAACAG 31466
Qy    55 ----------------------------------------------------------------    54
Db 31465 CAAAGGAGTGAGCCAGGTGGATATCCAGGGGCAGAACTGTTAAGGCAGAGAGGAAACAGCAT 31406
Qy    55 ----------------------------------------------------------------    54
Db 31405 GAGGGAACAGCCGTGTGCAAAGGCCTGGGAGTTGGGAGTGTGGCTGGGGGTGCTTCCAGGAAGG 31346
Qy    55 ----------------------------------------------------------------    54
Db 31345 GCAAAAAGTCCTGTGTGGGATGGGAGGATATGGGGAGCAAGGAGGAGTGGGTCAGATTGG 31286
Qy    55 ----------------------------------------------------------------    54
Db 31285 GTAGGGCCCTTGGGTGGTTGATTGTGTAAAGACTCTGGAGTTTAGACCAGGCACAGTGCCTCAGG 31226
Qy    55 ----------------------------------------------------------------    54
Db 31225 CCTGTTAATCCAGCACTTTGAGAGGCGGATCACCTGAGGTCAGGAGTTCG 31166
Qy    55 ----------------------------------------------------------------    54
Db 31165 AGACCAGCCTAGCCAACACATGGTGAAACCTTCGTCTCAACTAAAAATACCCAAAAATTAACCAG 31106
Qy    55 ----------------------------------------------------------------    54
Db 31105 GTGTGGTGGCACAAACCTGTAATCCCAGCTACTCTGGAGGCTGAGGCAGGAGAATCGGCTT 31046
Qy    55 ----------------------------------------------------------------    54
Db 31045 GAACCCGGAAGGTGGAGGTTGCAGTGAGCTGAGATTGTGTCCACTGTACTCCAGCCTGGGT 30986
Qy    55 ----------------------------------------------------------------    54
Db 30985 GGCACCATAAGACTCTGCCTCAAAATAAAATAATAAAATAATAAAGACTTTTGAGTTTCCT 30926
Qy    55 ----------------------------------------------------------------    54
Db 30925 GGAGTGAGAGGAGAAGCCCTTAGAGGGCTTAGCAGGGAGATGAACATGATCTGATTTTCATT 30866
Qy    55 ----------------------------------------------------------------    54
Db 30865 TTTAATCCTTCCTGCTATGTGTGAAGAATGGACTGAAGGCAAGGTGTTTTGTATATTTGTCT 30806
Qy    55 ----------------------------------------------------------------    54
Db 30805 GTTTCGTAGAGACACAGGGTCTTGCTCTGTTGGCCAGGCTGAAGTGCAGTGGCACAATCACG 30746
Qy    55 ----------------------------------------------------------------    54
Db 30745 GCAGCCTTGAACTCCTGGGCTCAGGCGAAACTCCCACTCACTCCTCCTTACTCTCACCAT 30686
Qy    55 ----------------------------------------------------------------    54
Db 30685 TGTGCCCTGCTAATTTTTTAAAAAATTTATTTTGTAGAGAATGGTGGTCTCTCACTATGTTGCC 30626
Qy    55 ----------------------------------------------------------------    54
Db 30625 TAGGCAAGTCTTAAATTCTCGGTCTCAAATGATTCCTCGCGATGTCCCAAAGTGCT 30566
Qy    55 ----------------------------------------------------------------    54
Db 30565 GGGATTACAGGTGTCAGCTGCTGCCATGCCCACCTGTATTTTTTTTTTTAATGGGGAAAAAG 30506
Qy    55 ----------------------------------------------------------------    54
Db 30505 CCTTTTAATTAGTATGAGGTGTTTTCGGTTGTTTTCTACCATAAAGCTCTTCTGTAAATCAA 30446
Qy    55 ----------------------------------------------------------------    54
Db 30445 AATAGAAATGTAATTATTGATAGAGCAATGACCTTAGACTACAGTGCAGACTTTTCATCT 30386
```

```
Qy    55 ----------------------------------------------------------------    54
Db 30385 TACATTTGGGCTCATGAATTTTAGTATAAACTGATTATGACAGTGTTTTTTACATAGTTAT 30326
Qy    55 ----------------------------------------------------------------    54
Db 30325 GATCTAGAGCGAGAACTGAAAACAAAATAACACATACTCTACATCAAATATATTCGTTCAGT 30266
Qy    55 ----------------------------------------------------------------    54
Db 30265 AATATCTGGGCTTGGATGAACCTGCAGAAGTAGGTAGGTAAAGCTGTCAGATATTTTCTTAAAC 30206
Qy    55 ----------------------------------------------------------------    54
Db 30205 CAACAGAAAAGAAAATGTATATGACAGATGTTGTGTTTACTTATTATTTATTTATTTATT 30146
Qy    55 ----------------------------------------------------------------    54
Db 30145 TATTTATTTTGAGATGGAGTCTCACTGTGTCACCAGGCTGGAGTGCAGTGGTGTGGATCTCT 30086
Qy    55 ----------------------------------------------------------------    54
Db 30085 GCTCACTGCAACCTCCACCTCCCGGGATTCAAGCGATTCTCCTGCCTCAGCCTCCTGAGTA 30026
Qy    55 ----------------------------------------------------------------    54
Db 30025 GCTGGGATTACAGGCGTGCACCACCACGCCTGGCTAATTTTTGTATTTTTAGTAGAGACA 29966
Qy    55 ----------------------------------------------------------------    54
Db 29965 GGGTTTCACCATGTTGGTCAGGCTGGTCTCGAACTCCTGACCTCGGGATCTGCCCACATC 29906
Qy    55 ----------------------------------------------------------------    54
Db 29905 AGCCTCCCAAAGTACTGGGATTACAGGCCATGAGCGCCACGCGCGCCTGTTATTTATTTT 29846
Qy    55 ----------------------------------------------------------------    54
Db 29845 TTTACCACTATGGAGTCCAATATGAAATTCTCACAACTAATGCAAATACATTATTAACATG 29786
Qy    55 ----------------------------------------------------------------    54
Db 29785 TAAGCACACCTAGGTATAAATATGCACATAGTCCATTAATTACATCAGGGGAATTAAAAA 29726
Qy    55 ----------------------------------------------------------------    54
Db 29725 CATACTTTCAAGTTAAAATGAATTTTCAGGAAAAAAACTGCATTCACAAAATCTGAAATGT 29666
Qy    55 ----------------------------------------------------------------    54
Db 29665 GAATACAAAAATGAAATTGTGAAATAAATAATATAGGTGTCACTNNNNNNNNNNNNNNNN 29606
Qy    55 ----------------------------------------------------------------    54
Db 29605 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 29546
Qy    55 ----------------------------------------------------------------    54
Db 29545 NNNNNNNNNNNNNNNNNNNNNNTATGACCATCCACTTGGGGCCAGGGGCTTTTGAT 29486
Qy    55 ----------------------------------------------------------------    54
Db 29485 CGCCTCCAGCTAATTAGGGTTCCAGTGAGCAGAGTGGCAAGCCCTGCCCTAATGAATA 29426
Qy    55 ----------------------------------------------------------------    54
Db 29425 ATGCCAGGGACTGGGCGGTGGGTACTTACAGTGTGCCCTTCATGGAACACTTTTTTTTT 29366
Qy    55 ----------------------------------------------------------------    54
Db 29365 TTTTTTTTGGAATGGAGTCTCGCCCTGTTGCCCAGGCTGGAGTGCAGTGGCACAATCTCA 29306
```

```
Qy      55  ------------------------------------------------------------  54
Db   29305  GCTCACTGCAACCTCGTCCTCCTGGGTTCAAGCAATTCTCGTCGTCCTCAGCCTCCCAGGTA  29246

Qy      55  ---  54
Db   29245  GCTGAGATTACAGCCCTGTGCCATCATGTTCTGCTCAATTTTTGCATTTTAGTAGAGACG  29186

Qy      55  ---  54
Db   29185  AGGTTTCACCAAGTTGGCCAAGACTGGTCTTGAATTCCTGACCTCAGGTGATCTGCCCAC  29126

Qy      55  ---  54
Db   29125  CTTGACCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGCGCCCGGCCCCATGAAATA  29066

Qy      55  ---  54
Db   29065  CTTCTTACCTGCGGGACAGCCTAATAGCTCAGTCGTGTCTAACCCATGCTCTGGGGGGTCTTC  29006

Qy      55  ---  54
Db   29005  ACACTTGTTTATTCTGGCAGACGTCCCTGTGACTCTTGTCTGATCCATGTCCAAGTTTAT  28946

Qy      55  ---  54
Db   28945  GCCTGTCTTGACCATTGCTCTGGGCGCTGGGCGAGCCCAGACTGTGTTCCAGCAACCCAGGGAA  28886

Qy      55  ---  54
Db   28885  AACCAGGCCTGGGCGTGGGGTTCCTGAGGATGGAAGGTGCAAATTCAGTACACCACC  28826

Qy      55  ---  54
Db   28825  TCAATGCAAAAACAAGTTCAAAAGCTTATTACTTACAGATCCTGAGCAGGGAAGGTGCAAT  28766

Qy      55  ---  54
Db   28765  GACTAGGGAGGGGTCATCCTCCATCCTGGGCTACATGAGAGCGGGAATGAAAGAGTCAGGCAA  28706

Qy      55  ---  54
Db   28705  AAAGAAAGTGAGAGCTTGTGGGCAATGAGAAGTATTATTATGTAAGGGACTAGGGTGTGGGT  28646

Qy      55  ---  54
Db   28645  CAGGTTAAGTTTGAGGGCAAATGCTTGAAATGATCCCTTTAAGGAAATGGGTGGGAAGTGG  28586

Qy      55  ---  54
Db   28585  GGAGCCCAAGTTTGCCGGGAGGAGAGATGCCTCGAAGTTCTTATCTCTGGGCCACTGGCTT  28526

Qy      55  ---  54
Db   28525  GGACCAATCTGAGTGTGGCATCTACTCTTTAAATCCTAGGCAGCGAACCTTTGCTGTGTCATC  28466

Qy      55  ---  54
Db   28465  TCCCTTACACAAGGTTGGAAGCAAGGAGGACCGGTCAGGAAGGCCTTTGGTGTGTAACCCATGT  28406

Qy      55  ---  54
Db   28405  TATTGTAATATTCATTACTCAAACGATGTTTATTTATGTGCACCTACTATGTGCTGAG  28346

Qy      55  ---  54
Db   28345  GCCATGGCAGGAGGCTTCGGGGGATGTGGCTTGAGAACAGGAGAGCCCCTGGTCGTCCTTGA  28286

Qy      55  ---  54
Db   28285  TATCCTCAAGGATGCTCCCTCCTGGAGGCCATTAGGTTCTTCCTGTTTCCATGTGTTGTTCTGCTG  28226
```

```
Db   28225  GAACCCTTCCGGGTCCCAGAGTGTGCAGGAGGCTTCCCCTGGCAAAGGGTCTTCTCTCAT  28166

Qy      55  ---  54
Db   28165  GGCACAAGGGCTTGGCAGCTACAGCCCAGTCAGTTACCTCCTGGTTCCTCAAACTCAGTGAGCAC  28106

Qy      55  ---  54
Db   28105  CTGCTTGCCCTTCGTTCGTTGCCCCTCAGCTTGGGATGGCCTGAGTCAAGACAGCAGGAG  28046

Qy      55  ---  54
Db   28045  CTCCAGGCTTCATGACCCCTTTCTTTCCCAGGGAGGCCCCGTCTGGCCCCTCCCCAGA  27986

Qy      86  ATGTGACGGCTGCTTCTCCCAGAACTTCAGCGTGTTACCTGACATGGCTTCCCAGGGCTTGGCA  145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27985  ATGTGACGGCTGCTTCTCCCAGAACTTCAGCGTGTTACCTGACATGGCTTCCCAGGGCTTGGCA  27926

Qy     146  ACCCCCAGGAGATGTGACCTATTTTGTGGCCTATCAG  180
            |||||||||||||||||||||||||||||||||||||
Db   27925  ACCCCCAGGAGATGTGACCTATTTTGTGGCCTATCAGAGGTAGAGGGGGGACTCTCTCGGCTGG  27866

Qy     181  ---  180
Db   27865  TGGAATGGGGAAGACTGAGGGGGGTGGGGGCTTGGAGGGGGCTGCAGACGCTGCAC  27806

Qy     181  ---  180
Db   27805  CCAGTGTGGGCAGCACTGGCTAGCTCTCTGGGGCCCTTACGGCGGGAGATGGCATGTGGCCGGCA  27746

Qy     181  ---  180
Db   27745  TTTGGGAGGGGGCTTTTGATAAAGGTCTGAGGTGGGAGACATGTTGAATGAAAGACAGT  27686

Qy     181  ---  180
Db   27685  GTACAGGTGACCAGTCTGCCGGGGGGGGAAGTCTTTGAGGAAAGTTGGTGTGGGGGCA  27626

Qy     181  ---  180
Db   27625  TGGATGTAGCTGCTGGGGGGCCAGAGGATGAAATTCTCAAGTGGGCTGGATGAGGTGCTTGGA  27566

Qy     181  ---  180
Db   27565  GCTGTGCCAGCTGATCAGTGAGGCAACTAGGTACACAGCAGAGGAGCTGTTACCTGGGCA  27506

Qy     181  ---  180
Db   27505  ATTAGGCATCCCTCAATGATCACACTTTTTTTTTCTCTTTTTTTTTGAGACAGAG  27446

Qy     181  ---  180
Db   27445  TCTTGGTCTGTGTCACCCAAAGTGGAGTGGCAGTGGCTTGATCTCTGGGCTCACTGCAACCTCCA  27386

Qy     181  ---  180
Db   27385  CCTCCTGGGTTCAAGTGATTCTCCTGCCTCAGCCTCCCAGAGTAGCTGGGATTACAGGCAT  27326

Qy     181  ---  180
Db   27325  ATGCCACCACATCTGGCTAATTTTTGTAATTTTAGTAGAGACGAGGTTTCTCCATGTTGC  27266

Qy     181  ---  180
Db   27265  CCACGCTGGTCTGGAACTCCTGAGCTCAGGTGATCCACCCACCTTCAGCCTCCCAAAGTGT  27206

Qy     181  ---  180
Db   27205  TGGGATTACAGGCGTAAGCCACCGGCGCTTGGCCAAATGTCACACTTTTCCCGATGGGAT  27146

Qy     181  ---  180
```

```
Db  27145 CATTCTCAATTTGGAAGCCCAGGCAGCCACCGGAAATCCAGAGAAATCTGACAAATGGGAAG 27086
Qy    181 ------------------------------------------------------------  180

Db  27085 CAGAATCCACCATCTTCGCACATAGATGGGAAATCGTTCAGAGTTCTTTAGCGGACACAGTGA 27026
Qy    181 ------------------------------------------------------------  180

Db  27025 GATGATAGAAGCAGAAGCTCGGGAGGAGATTCACCTGGAGTTGGTGAGGAGGGAAAGCAGG 26966
Qy    181 ------------------------------------------------------------  180

Db  26965 AAGAGGAGGGGGACCACCGTGTTCCTCAGGACCCGTGTCCCAGGCCAAGTGCTAAGGGC 26906
Qy    181 ------------------------------------------------------------  180

Db  26905 CCTACGTGAATATTTCACTTCCTTCTCCCAAATGTGACCAGGCAGCGCTCTGTGTTTCCCC 26846
Qy    181 ------------------------------------------------------------  180

Db  26845 ATTCTAGAGGTTGAGGGGATTCAGCTTCAGAGAGGGTGCTGTGTGTCTCTGAGGAGGACGTC 26786
Qy    181 ------------------------------------------------------------  180

Db  26785 ATGGAGCCAGAAGGGGAACTCGGGTTCCGACTCCAACATTTGTGCCCTTCCTGTTGCATCA 26726
Qy    181 ------------------------------------------------------------  180

Db  26725 CGTCATCCTTCCATGTGTGGAATCCACACATGTGAGTGATGGGAGCCTGGGCTTGAGCAGGGA 26666
Qy    181 ------------------------------------------------------------  180

Db  26665 CAGACTGCAAGAGAGCGTTTCAAAAGCGAAGAGCGTTTATCAGTTGCCAGAAAACACCTAATA 26606
Qy    181 ------------------------------------------------------------  180

Db  26605 TTTACTGTGTGGGCTGGCACTGTGTCAACACATGTAATGAACTTAATCTCACACGCAGCTCT 26546
Qy    181 ------------------------------------------------------------  180

Db  26545 CTGAGGACAAGTCACACAGCTGGGCGCGTAGTATGGCTGGAATAAAATTATTAAGGAGTTGA 26486
Qy    181 ------------------------------------------------------------  180

Db  26485 GTTGCTCAAAGTCACACAGCTGGGCGCGTAGTATGGCTGGAATAAAATTATTAAGGAGTTGA 26426
Qy    181 ------------------------------------------------------------  180

Db  26425 AAGTCTATCCTCTAGGACCAAGCATGGTGGCTTACATCTGTAATCCCAGCACTTTGGGAG 26366
Qy    181 ------------------------------------------------------------  180

Db  26365 GCCGAGGTGGGGGGGAGAATTGCTTTGGGGTCCTTTATTTCTNNNNNNNNNNNNNNNNNN 26306
Qy    181 ------------------------------------------------------------  180

Db  26305 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 26246
Qy    181 ------------------------------------------------------------  180

Db  26245 NNNNNNNNNNNNNAACACAGAGCCAAGAGATCCTAAAAAGAAGAAAAGTCTATC 26186
Qy    181 ------------------------------------------------------------  180

Db  26185 CTCTGAACTTCTATGATATTTTCATGTCTTTTATACATTAGAATGGTGATATTCTAATT 26126
Qy    181 ------------------------------------------------------------  180

Db  26125 ATATAATTTTTTCATTGTTAGTTGGAATTATTTATAAAGAGATGTATCCTCTCATCT 26066
Qy    181 ------------------------------------------------------------  180

Db  26065 GGTATTTGATATCCAGTCATACTATTCAAATAGGCAAGAGAGGTAAATCCTTAATTTTTT 26006
Qy    181 ------------------------------------------------------------  180


Qy    181 ------------------------------------------------------------  180
Db  26005 TTCCTTTATCAATTTTCAAGATAATGAATTGGTTCCTTATCAATCTCCAAAAGGTGATTGC 25946
Qy    181 ------------------------------------------------------------  180

Db  25945 TAGTTTATTATTATCATTTATGAACTCAGGCATTAAACACATTGGTGGTTTCAGTCTAT 25886
Qy    181 ------------------------------------------------------------  180

Db  25885 TGCGACGTACTCTGCTCATTGAAGCTTGAATTGCCTCATCTCTGTCCAGTGGGAGTCTCA 25826
Qy    181 ------------------------------------------------------------  180

Db  25825 TCAAGTTTGCTCCTGAGTCCTTTTAACTTGACCCTAGTGGTCAAGTTAAATCTTTCCAGA 25766
Qy    181 ------------------------------------------------------------  180

Db  25765 TTTAACAGATACCTTTCCAGCGTGTCCATTACGACAAGAAGTGTTCCAGTGTCCCTCTGGTACA 25706
Qy    181 ------------------------------------------------------------  180

Db  25705 ATTCCTGACCTAAAAACCTGCAGTCAGCCCATTTCTCATTAGTAAGAAATGGTTATAAAG 25646
Qy    181 ------------------------------------------------------------  180

Db  25645 ACTATAATCTGCATGCTAGCCTATGCCTGATCACTCACTACTTAGCTATTGCTTTTGGTGTTTTCA 25586
Qy    181 ------------------------------------------------------------  180

Db  25585 GTGAACAGAGTGATGTGTGTATACCATAGACACACATGTACTACATACTTTTTTTTTTT 25526
Qy    181 ------------------------------------------------------------  180

Db  25525 AGACAGAGCGTTCACTCTGTCACCCAGAGTGCAGTGGCATGATCTCGGCTCACTGC 25466
Qy    181 ------------------------------------------------------------  180

Db  25465 AACCTCCACCTCCTGGGTTCAAGAGATTATCCTGCCTCAGCCTCCTACTAAGTAGTTGGGATT 25406
Qy    181 ------------------------------------------------------------  180

Db  25405 ACAGGCGCCCACCACCATACCCGGCTAATTTTTGTATTTTTAGTAGAGACGGGGTTTCAC 25346
Qy    181 ------------------------------------------------------------  180

Db  25345 CATGTTGGCCAGGCTGGTGTCGAAACTCCTGACCTCAAGTGATCTGCCCCCTCGGCCTCC 25286
Qy    181 ------------------------------------------------------------  180

Db  25285 CAAAAGTGTGGGATTACAGGCATGAGCCATCGCACCAGCCTACATGTACATAATTTTTA 25226
Qy    181 ------------------------------------------------------------  180

Db  25225 AGATAAAATGCCTAATGAGTTATACGGGGTGCTTCCCATCTAAATTTAGTTCCTTAGGATT 25166
Qy    181 ------------------------------------------------------------  180

Db  25165 TTTACCTGACTTCTATGGTACATCTATATTTTCTTTTCACACTGAGAATCCTGTTTC 25106
Qy    181 ------------------------------------------------------------  180

Db  25105 TCAAGGACAGGGGACATGAGAACTAGAAATGACCCAATAATTACTCAATTTTCTTTATCC 25046
Qy    181 ------------------------------------------------------------  180

Db  25045 AAAACATACATACTTGCCTCTTAAATAGTTTCTTTCGCCCAAAGGGTTTGTGAT 24986
Qy    181 ------------------------------------------------------------  180

Db  24985 GGTCAAATAATTAGGTGTCAACTTAATTGGGTTGAAGGATGCCTTAGACGATGGCTGTTAAAGTTT 24926
```

```
Qy    181  ------------------------------------------------------------  180
Db  24925  TGTTTCTGGGGGTGTTCTGTGTGAGGGTGTTGTCCAGAGGAGGAGACTGACATTTGAGTCAGTGGAC  24866
Qy    181  ------------------------------------------------------------  180
Db  24865  TGGGAATGAAAGAGACTCGTCCTCACTGTGTGGGGTGGGGCACAACCAAACTGGCTGCCAGG  24806
Qy    181  ------------------------------------------------------------  180
Db  24805  CTGGCTGGGAAAGCAGGTGGGCAGAGATGGGTGGGGATAGCTTCACTTGGCTTCCAGCTTC  24746
Qy    181  ------------------------------------------------------------  180
Db  24745  CTTCTTCTTCCCGTGCGGGGATGCTTCCTTCTGCTCCTCCCCTTGAACATCACACTCC  24686
Qy    181  ------------------------------------------------------------  180
Db  24685  GGGTTTTTTTGGCCTTTAGACTCTTGGACTTAAGTTAGTGGTTGGTTGCTGGGGGGTCTCTCGGAT  24626
Qy    181  ------------------------------------------------------------  180
Db  24625  CTTTGGTCACAGACTGAAGGCTGCCACTTTCAGCTTCCCTGGTTTTGGACGGTTTCAGATTC  24566
Qy    181  ------------------------------------------------------------  180
Db  24565  GGACTGAGTCACTATGGCTTCTTCTTTCTTCCCACACTTGCTGACGGGCCTTATCGTGGGGGACTTC  24506
Qy    181  ------------------------------------------------------------  180
Db  24505  GCCTTGTGATCGTGTGAGCCAATTCTCCTTAATAAACTCCCTTTCATATATACGTATAAC  24446
Qy    181  ------------------------------------------------------------  180
Db  24445  CTATTAGTTCTGTTCCTCTGGAGAACCCTGACTAATAAAAGGGTTGTTGCTTTTTCTTTAA  24386
Qy    181  ------------------------------------------------------------  180
Db  24385  AATCTAGTAATTTATTTTATTTGACTGTGTTGGTATTGCTCATTCATTCTGACTTGATATTT  24326
Qy    181  ------------------------------------------------------------  180
Db  24325  TTAGGCACTCAATATTCTCACTTAATACATGGTTCCAAGGCATTTTTATTTTAGGAAGGT  24266
Qy    181  ------------------------------------------------------------  180
Db  24265  TTTCTTAAATATATAGTTTTAGTATTGTTCTATTCTCTGTTTTGATTTCTTCTTTAGG  24206
Qy    181  ------------------------------------------------------------  180
Db  24205  GACTCATATCACTGTATGTTGGATCTTCTTTTTCGTGTTCAGTATTTGTCTTTTGGGC  24146
Qy    181  ------------------------------------------------------------  180
Db  24145  ACAGAGACTCACACCTATAATTCCAAGACTTTGTGAGGCATAGGTAGGAGGATCGCTTGA  24086
Qy    181  ------------------------------------------------------------  180
Db  24085  GCCCAAGAGTTTGGAGACCAGCCTGGGCGCAACATGGTGAGGCCCTGTCTGCCAAGTTAAAGAAA  24026
Qy    181  ------------------------------------------------------------  180
Db  24025  AAGGAGAGAAATACTTGTCTTTTTCTTTCAAAATGCCTTTTATCGTGTCTATCTACTATCTACTAT  23966
Qy    181  ------------------------------------------------------------  180
Db  23965  TCTGCTCTCTAAATGAAAATAGGTTTCACTCTTGAGTTTTTAAAAAACTGTATGCTTCCAT  23906
Qy    181  ------------------------------------------------------------  180
Db  23905  GTGTGAGAATTATTCAACATCTTATTTGTAATCTTTCTCTTGGTTACATTTATTTTTCCTG  23846
```

```
Db  23845  AAACTCTAGTCTGCTTTAGCTGACATGTTTGTTGTAGCTAAGAGCGCACATTTCTTATCATA  23786
Qy    181  ------------------------------------------------------------  180
Db  23785  GCTTGCCGTGCTGGAATTAAATTCCAATTTTCTTTTAAAACCAACATTATTGAGTTAAAATG  23726
Qy    181  ------------------------------------------------------------  180
Db  23725  TATATAGAAATAAAACTGTTCCCATTTTAAAGTATACAATTTGAATGAGTTTTGACAAAAGTG  23666
Qy    181  ------------------------------------------------------------  180
Db  23665  GGCACCCACGTACCCACCACCACAATCAAAGATGTAAGGACGTTCTCTATCACCCCAGAAAG  23606
Qy    181  ------------------------------------------------------------  180
Db  23605  TTCCCTCATCCACTTTGCATTCAGGCCTCCAGATCTAGGCAACCACAGATCTGCTTTCTG  23546
Qy    181  ------------------------------------------------------------  180
Db  23545  ACACTGTGGATTAAACTTTGCCTGTTCCAGAATTTCATATAAATGGATGTGTATAGTATG  23486
Qy    181  ------------------------------------------------------------  180
Db  23485  TACCCTTTCGTGTCTCTGGCTCCTTTCCCTCAGCCATAAAGTGTTTCTGAAAATTCACCCACATTG  23426
Qy    181  ------------------------------------------------------------  180
Db  23425  TTACAGTTATCAGTAGTTAAATTCCTTTTTATTGCTGAGTAGTAATGCCATTGTATGACTA  23366
Qy    181  ------------------------------------------------------------  180
Db  23365  TGTATGACATTTGTTAATCCATTTCCCGTCAGTGGATATATTTGGGTTGCTTCCAGTTCTG  23306
Qy    181  ------------------------------------------------------------  180
Db  23305  GGCAGGGTATTCATTTGCTAGGGGCTGCCATATGCTTGCCCTCTGGCCTCCCAAAATTGTG  23246
Qy    181  ------------------------------------------------------------  180
Db  23245  TCCTTTTCATATGCAAAATACATTCACCCCTCCCAACAGCCCCAAAACTCTCTTTTTT  23186
Qy    181  ------------------------------------------------------------  180
Db  23185  TTTTTTTTTGAAACAGAGTTTTGCTCTTGTTGCCCAAGCTGGAGTGCAATGGTGTGGATCT  23126
Qy    181  ------------------------------------------------------------  180
Db  23125  CGGCTCACTGCAACCTCTGCCCTCCCGGGTTCAAGAGAATTCTCCTGCCTCAGCCTCCTGAG  23066
Qy    181  ------------------------------------------------------------  180
Db  23065  TAGCTGGGATTACAGGCATGCGCCACCACGCCTGGCTAATTTTTTGTATTTTTAGTAGAA  23006
Qy    181  ------------------------------------------------------------  180
Db  23005  ATGGGGTTTCACCGTGTTAGCCAGGCTGGTCTTGAAACTCCTGACCTCAGGTGATCGGCCT  22946
Qy    181  ------------------------------------------------------------  180
Db  22945  GCCTTGGCCTCCCAAAGGGCTGGGATTACAGGCGTGAGCTACCACGCGCTAGCCCCA  22886
Qy    181  ------------------------------------------------------------  180
Db  22885  AAACTCCTTAACCCATTTCAGCATCTTAAGTCCAAAGTCTCATCTAAATCAGGTATG  22826
Qy    181  ------------------------------------------------------------  180
Db  22825  GGTGTGGACTGGGAGTGTTACTCATCCTGAGGCCAAATTCCTCTCCACTTATGGAACCTGTG  22766
Qy    181  ------------------------------------------------------------  180
```

```
Db  22765  AAACCAGACAGGTTATGTGTCTTGAAAAATAAAGTGATGGGACAATGCATGGGAATAGACTTT  22706
Qy    181  --------------------------------------------------------------    180

Db  22705  CCCATTCCAAAAAGAGAAAAATAGGAAGAAGAGAGAAAGAGAAGTGACAGGTCCCAAGCAAGTCTA  22646
Qy    181  --------------------------------------------------------------    180

Db  22645  AAACCTCGGCAGGGCAAAATTCCATTAGATTTTAAGTTCAAGAATAGCCCTCTTTGGCTCA  22586
Qy    181  --------------------------------------------------------------    180

Db  22585  GTGCTCTGCCCTTTGGGCCCCACTGGGCGGGCGGCAGCCCTATCCCCTTTGCCCTGGGTGGTGA  22526
Qy    181  --------------------------------------------------------------    180

Db  22525  CCCTACCCTCGAGTCACTGGTTAGCAGCACCTTAGCCCTGCTGAAACTAAGGAGGGGACAG  22466
Qy    181  --------------------------------------------------------------    180

Db  22465  TGTTGCCTCCAGGTCTTTGGTGGGCAGTGACAACCCTGCTGATCTCTGAATCATCTTCCAG  22406
Qy    181  --------------------------------------------------------------    180

Db  22405  GAAATTTTCCCTATACTTGAAGGATATTGCGTGTTCACAGCCAAAATAGCTCCAGCTCTT  22346
Qy    181  --------------------------------------------------------------    180

Db  22345  GTCCCTTTCTTTAGAAATCCCAGAAGTCCAACAGCCTTCCTTCATTCTGTCCCATCTCTGT  22286
Qy    181  --------------------------------------------------------------    180

Db  22285  CCCCTTTAGTCAAAGCTGGAAGTGCCTCTTGCTGGTATAATCCATCAGTATGTCTAATTT  22226
Qy    181  --------------------------------------------------------------    180

Db  22225  CTGCTTAAATGGCTGATTAAGTCTATGAGTTGCACCTCTGATCTCTTTTATCAAAAGGTTG  22166
Qy    181  --------------------------------------------------------------    180

Db  22165  TTCTAGCCACAACCTTAGTGTGTCTCCCCAGAACATGCTTCTCATTTTTTTTTTGCAAT  22106
Qy    181  --------------------------------------------------------------    180

Db  22105  GTGGAATAGGCTGAAAATTTTCCAAAAGCTTCAAGTTCTTAGTTCCCTTTTGGCTTACCAATTC  22046
Qy    181  --------------------------------------------------------------    180

Db  22045  TTTTCATATATCTCTTCTCTCACATTTACTATAAGCAGTAAGAGAAAACCAGGTTGTAC  21986
Qy    181  --------------------------------------------------------------    180

Db  21985  CTTCAGCACTTTGCTTAGAAATCTCTTCTGCTAAGCATCCAAGTTTATGTCTTTTAAATT  21926
Qy    181  --------------------------------------------------------------    180

Db  21925  ATCTTTTTGTTATTATTATTTATATATCATTTTTGAGATGGGCTAGCCAAATGAACTTTTA  21866
Qy    181  --------------------------------------------------------------    180

Db  21865  CTTCTAATTTCTGCAAAAACACTAGAGACAAATCAACCAGTTCTTTGCCACTTTATAAACA  21806
Qy    181  --------------------------------------------------------------    180

Db  21805  AGGATCACCTTTCCTCCAGTTTCCAATAACACATTCCTTCTTTTCCACCTGAGACCTCACC  21746
Qy    181  --------------------------------------------------------------    180

Db  21745  AGAATCACCTTTAATGTCTATAATTCCTACCAATAGTCTTTTTAAGGCAATATAGGGCTTTC  21686
Qy    181  --------------------------------------------------------------    180

Db  21685  TCTAACAATGCACTTCAAACTTCAAGAATTCTACCCATTATGCGAATTCCAAAGCCACTTCCA  21626
```

```
Qy    181  --------------------------------------------------------------    180

Db  21625  CATTTTTAGGTATTGATTACCTTCAGCACCTTCAATTCTCTGGGTGCCCAAATCTCACTGGGTTT  21566
Qy    181  --------------------------------------------------------------    180

Db  21565  GCTAGGGGTCTGCCATAACAAAGTACGACAGTCTGGGGTAAACACAGAGAATTTTATTTCTCA  21506
Qy    181  --------------------------------------------------------------    180

Db  21505  AAATTCTGGAGGTTGGAAGTCCAAGGTCAAGGGCGGTTGCTAGGGTTAGTTTCTCCTGGAAGC  21446
Qy    181  --------------------------------------------------------------    180

Db  21445  CTCTCTCCTTGGGCTAGCAGATGGGCTGCCTTCTTCTTGCGTGTCTTCAGGTGGCTTTTTCTCT  21386
Qy    181  --------------------------------------------------------------    180

Db  21385  GTGTGTGTTCACTCTGGTATCCTTCCTCTTCTTACAAGTACACCAGTCCTACTGGATTA  21326
Qy    181  --------------------------------------------------------------    180

Db  21325  GGGCCCCAGCCTTATTACTTCATTTAACCATAATAACCTCTTTATCTCTTATCTCAAA  21266
Qy    181  --------------------------------------------------------------    180

Db  21265  ACACAATACCACTGGGGATGAGGTCTTCAACATATATGAAGTCAAATTCGTC  21206
Qy    181  --------------------------------------------------------------    180

Db  21205  CATAATAGGGCTAATTATGAATTAAGCTGCTGTGAACATTCATGTACAAGTCTTTGTGTGG  21146
Qy    181  --------------------------------------------------------------    180

Db  21145  ATATGTTTTCATTTCTCTTAGATAAAGATCTAGGAGTATATCAGCCTGGCAACATAGTGAG  21086
Qy    181  --------------------------------------------------------------    180

Db  21085  ACCCCACCTTTACAAAAATTTCAAAAATTAGCCAGGCATGGTGGCACACCTGTAGCC  21026
Qy    181  --------------------------------------------------------------    180

Db  21025  CTGCCATCTCAGGAGGCTGAGGTGGGAGGATCCCTTGAGCCCAGGGGGTTTAGACTGCAG  20966
Qy    181  --------------------------------------------------------------    180

Db  20965  TGAACTATGATTGCACCACTGCACCCCAGCCTGGGTGACAGAGTGAGACTCTGTCTCTAA  20906
Qy    181  --------------------------------------------------------------    180

Db  20905  AAAAAAGAGAGAGGGGAGGAAGGAAAAGAGAGAGGGAGGAGGAGGGGAG  20846
Qy    181  --------------------------------------------------------------    180

Db  20845  GGAGGAGGAGAGAAAAATGGGATCCTAGGGTTAAGATTTAGGGAGAATTAGGGTAATGTGTA  20786
Qy    181  --------------------------------------------------------------    180

Db  20785  CTATTACAGGGGGAACTGTGGAGCTGTTTCCAAAGTGACTGTTACCAATTGTTCAATTGCCACCA  20726
Qy    181  --------------------------------------------------------------    180

Db  20725  ACAATACATGAGAGAGTTCTAGTTACTCCATGTGCTTGTTACACTTAGTATTATATCAGTCTTT  20666
Qy    181  --------------------------------------------------------------    180

Db  20665  TTCATTTAACCATTCTAGTGAGTATGTAGTAGTATTTATTATGGCTTTAATTTACAC  20606
Qy    181  --------------------------------------------------------------    180

Db  20605  TCCCTAATGATGAATGAATGTTGAACATCTTTCATGTGCTTATTGGCATTCATATATCT  20546
```

```
Qy    181  --------------------------------------------------  180
Db  20545  TTTGTGAAGTGACTATTCAAATATTTTTCCACTTTTTATTTATTTCTTATT  20486
Qy    181  --------------------------------------------------  180
Db  20485  ATTGAGTTATCTATGAATACAAAATCCTTTATCAGTGTATGTATGATTTTTTCCCCA  20426
Qy    181  --------------------------------------------------  180
Db  20425  GTGGCTGGCCCTTTCATTTCGTTAGGCTTTTTTGGTGGGTTTTTTTTTTTGGAA  20366
Qy    181  --------------------------------------------------  180
Db  20365  GAGAAAATATTTTAATTGATAAAATCCAGTATATCAGTGTTTATAGACTGAATTATAC  20306
Qy    181  --------------------------------------------------  180
Db  20305  TCTACCCCACAAATTCATATGTTGAAGCCCTAACCTCTAAGTGACTGACTATTTGGGAGATGAGC  20246
Qy    181  --------------------------------------------------  180
Db  20245  CTTTAAGGAGGTAATTAAAGTAAAATGAGATCATTAAGGGTGGGCCCTAATCTAATAGGAC  20186
Qy    181  --------------------------------------------------  180
Db  20185  TGGGTGTCTTTTATAGAAGAGGAAGACACCAAGAGCGCATGCAACACAGAGAGAACGGCCTTG  20126
Qy    181  --------------------------------------------------  180
Db  20125  TGAGGACACAGCAAGGATGAGACGGCCATCTGCAAGCAAGGAGAGGAGGCCTCAGTAGAAACC  20066
Qy    181  --------------------------------------------------  180
Db  20065  AAACCTGCTGAATGCCTTGATCTTGGACTTCCAGCCTCCAGATTTCTGTTGCTGAAGCCAC  20006
Qy    181  --------------------------------------------------  180
Db  20005  CCTGCCTGTGGTGTCTTACCATGGCAGCCCTCACGACTAATATAATCACAGATTTTTTTTCCT  19946
Qy    181  --------------------------------------------------  180
Db  19945  TCAACAGTTAAACGCTTTTGGTGTCCTAAGCCAATATTCGGCTGACCCAGGGTCATGAAGAT  19886
Qy    181  --------------------------------------------------  180
Db  19885  TTTTCTTCTTCTTATGCTTTCTTCTTCTGGAAGTTCTATATAATTTTTTTTTTAAC  19826
Qy    181  --------------------------------------------------  180
Db  19825  TTTCCTTCTTCTTCGCCTTCTGTTTCTTTAAGGCATCATCTATGTGTTGTTAATTTGTTCTT  19766
Qy    181  --------------------------------------------------  180
Db  19765  GTATTCCTTCGTGATTAATCTTCACTTCTGAAATGAATTTGCTTTTTAAAAATATATAT  19706
Qy    181  --------------------------------------------------  180
Db  19705  AATTCTTTTTCTGTGTCTGAGTTTTTCTAATTAGGTTTATGTGGGTTTTTTCTTGTCCTGC  19646
Qy    181  --------------------------------------------------  180
Db  19645  ATCACTTTTTACTCTTTTGCCCATTTTGACTGAGTCAGGTTCCAGTTTTGGATCTGTTCA  19586
Qy    181  --------------------------------------------------  180
Db  19585  TGGATATGTTTTTGTGACATGTTCTTCTCGGCTTCTTTATCATTTATTGCTTAGCTTATTA  19526
Qy    181  --------------------------------------------------  180
Db  19525  ATTTCTTATTCTTTCTTATTTCTATTATTAAGTATTTAAAGCTATATATGTTTTCCTTCTAAGT  19466

Db  19465  ATTACTTAGCTGTCTTATACGTTTTCATTTGTTGTTATTTGGTGATCATTTCAGCT  19406
Qy    181  --------------------------------------------------  180
Db  19405  ATTTAATTAATTTCCATTAATGATAATCTTTCAATCTATGGGGTTGTTTTAAAAATATTTTAAG  19346
Qy    181  --------------------------------------------------  180
Db  19345  GCCAGGTGGGTGGACTCACATCTGTTAATCACAGCACTTAGGGAGGCTGAGGTGGGAGGAT  19286
Qy    181  --------------------------------------------------  180
Db  19285  TGCTTGAGGCCAGAAGTTTGAGACCGGCCTAGGCCAACAAAGTGAGACCCCTCTTCTACAG  19226
Qy    181  --------------------------------------------------  180
Db  19225  AATATTTTTTAAAATTAGCTGGGCCAGGAGTGGTGGCGTCATCCCAGCACCTGTAATACC  19166
Qy    181  --------------------------------------------------  180
Db  19165  AGCACTTTGGGAGGCCAAGGCAGGATCACTTGAGGTTGGGAGGTCAGGAGGATCAGCCTG  19106
Qy    181  --------------------------------------------------  180
Db  19105  GGCAACATGGTAAAACCCCATCTTTACTTAAAATATAAAATTAGCCAGGTGTGGTGGTAG  19046
Qy    181  --------------------------------------------------  180
Db  19045  GTGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATTCTTTGAACCCAGGAGG  18986
Qy    181  --------------------------------------------------  180
Db  18985  AGGAGTTTGCAGTGAGCCGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCGAGA  18926
Qy    181  --------------------------------------------------  180
Db  18925  CTCTGTCTCAAAAAAAGAAAAGAAAAGAAAAGAAAAGAAAATTAGCTGGGTGGTAGTGGCAGGTACCTGTGG  18866
Qy    181  --------------------------------------------------  180
Db  18865  TCCCAGCTGACTCAGAGACTGAGGCAGGAGGATCACTTGAGCCCAGGGAGTAGAGGCTGCAG  18806
Qy    181  --------------------------------------------------  180
Db  18805  TGAGCTATGTTGGTGCCACTGCACTCCAGCCTGCGAACAGAGCAAGACGTCTGTCTCAAA  18746
Qy    181  --------------------------------------------------  180
Db  18745  AAAATATATATTTTTTTAAATTTCAAACTTCCTTAGTTCTCTTTTGTTATTAACTTTT  18686
Qy    181  --------------------------------------------------  180
Db  18685  AACTGAATGTTTTGCAATCAGAAGAAATACTTTATGAGATACCTATTCTTTAAAAATTCT  18626
Qy    181  --------------------------------------------------  180
Db  18625  TAAGAATTGCTTTGTGTTAATTAATATTTGTTAATTAGTTCACATGGTTCACCAATTTGTT  18566
Qy    181  --------------------------------------------------  180
Db  18565  TAGTTAGTTCTTTGTATATGTTGATTAGACCAAACTGATAACTGTGTGTTCTTTTATTTATT  18506
Qy    181  --------------------------------------------------  180
Db  18505  TATGTATTTATTTTTCTTGTCTATTCATCAATTGCTGGGTGAGATGTATTAAAAATTTCT  18446
Qy    181  --------------------------------------------------  180
Db  18445  TGTTGTAAGTGTGGGCTGTTCACTTTCTACCTGTAGTTTGTCTGTTTGCTTTATAGAGGGT  18386
Qy    181  --------------------------------------------------  180
```

```
Db  18385  GAAGTTGTTTAGTTAGGCACACATAAGTTAGAATTTTTCTGTCTTCCTGGTGAATGGAATC  18326
Qy    181  ------------------------------------------------------------    180

Db  18325  ATTTATCATTATTCTTCTTTTCATCTTTAGTATTGCTTTGGAAGTCTGTA            18266
Qy    181  ------------------------------------------------------------    180

Db  18265  TTTTGTCTCCTGTTAATATAAACTACACTGGTTCCTTTGGTGTGTGAATATTTGCATAGTATA  18206
Qy    181  ------------------------------------------------------------    180

Db  18205  ACATTTTCCATGAAGAAACAAAACAGGAGAATTGGTTCTTTCTCAAAATCTGATCTTTGT    18146
Qy    181  ------------------------------------------------------------    180

Db  18145  GTCAGCCCCATCTCAGCCTTCTCCATTCATCCTTGGTCACTCCCCAAACCCAGGAGCAA    18086
Qy    181  ------------------------------------------------------------    180

Db  18085  TCCTTGAATTCTCCTTTTCCCACATTCTACATCCAAATCGTTAGCAAGTTCTATTAGTTC    18026
Qy    181  ------------------------------------------------------------    180

Db  18025  TATTATTACCTCCAAAATAGATATTGAATCCAGCCCTTTCTCACTGTTCTCCACCATCATC   17966
Qy    181  ------------------------------------------------------------    180

Db  17965  CTGTCTCACATCCTTACCCATGGCCTCCTTGCTCTGGTTTGACCAGATGAGTCTTGTAAAAACA  17906
Qy    181  ------------------------------------------------------------    180

Db  17905  TGTTAGGCCAGGCACAGGTGGCTCCTGCCTGTAATCCCAACACTTTGGGAGGCCAAGCGGG   17846
Qy    181  ------------------------------------------------------------    180

Db  17845  TGGGTTCACCTGAGGTCAGGAGTTCGGAGACCAGCCTGGCCGACATGGTGAAACCCTGTCTC   17786
Qy    181  ------------------------------------------------------------    180

Db  17785  TACTAAAAATACAAAATTAGCCAGGTGTGGTGGTTACGGCTGGTGTAATCCCATCTTACTGGG   17726
Qy    181  ------------------------------------------------------------    180

Db  17725  GAGGCTGAGGCAGGAGAATCACTTGAACCCGAGGAGGTTGCAGTGAGCCAAGATC         17666
Qy    181  ------------------------------------------------------------    180

Db  17665  ATGCCACTGCACCCCAGCCTGGGCAACAAGAGCTCCATCTCAAAAAAATAAAAAAATTA      17606
Qy    181  ------------------------------------------------------------    180

Db  17605  AAAATAAAAATGTTAGGCTCCCTGGGCTCTCTGGCTTAGTCCATTTGTACTGCTTTAACAAA   17546
Qy    181  ------------------------------------------------------------    180

Db  17545  TACCTTAGAATGGTGTAATTCTATTATATAAATAATAAGCAATTAATAAATA            17486
Qy    181  ------------------------------------------------------------    180

Db  17485  ATAGCAATTCCTTCTCACAGTTCTAGAGGCTGGGAAGTTCAGGGTCAAGGTGGGCACCTG    17426
Qy    181  ------------------------------------------------------------    180

Db  17425  ACTCCGTTCTGGTAAGGGGGGCCTCTCTGCTTCCAAGATGGGTGCCTTCTCGCGTCTTC     17366
Qy    181  ------------------------------------------------------------    180

Db  17365  GCATAGCCGCAAGGGGCAAACACTGTGTCTCTCAGCTGGGCAGAGAGAGATAGAAGGGACCAGGCA  17306
Qy    181  ------------------------------------------------------------    180

Db  17305  GCTCTCTGAAGTATCCAGTTGGAGTCATGGAACTGCGATGTTCCCTCTGACATCCACAG    17246
```

```
Qy    181  ------------------------------------------------------------    180
Db  17245  AGTACCTTATCATGGTCCCTTGGCATGCAGCCAGGTGGCCCATAAACGCTGAAATGAAACAAC   17186
Qy    181  ------------------------------------------------------------    180
Db  17185  ATATAGTAATTGGTCGCTAGTACTTAGGAATTAGAGCATCACCGCAACAGTCCTGTGAGGGAGG  17126
Qy    181  ------------------------------------------------------------    180
Db  17125  CATTACAGATGAGGAAACTGAGGTTTAGGGGCAAGGACCTGCCCATGGTCCCAAAGCTAG   17066
Qy    181  ------------------------------------------------------------    180
Db  17065  GGAGGGACAGGGGTGGGGGATTCCCACTCCCATCCATCCTGGCTCCAGAACCTGAGCTCCTGA   17006
Qy    181  ------------------------------------------------------------    180
Db  17005  CCAGGCTGTTCTTTATCCCGTGTCTCAGCCAGTGGGCTGCCTGTCTTCTGGACCGGATGGACCTAAAG  16946
Qy    181  ------------------------------------------------------------    180
Db  16945  TCAGTCCAGCCAAACACAGAGGGAAGCAATGATCAACTGTTCTCTTAAGTTCCCTGACCCGGAG  16886
Qy    181  ------------------------------------------------------------    180
Db  16885  AGGCTGAGTCCATGGCCCAAGCTCCTCCTCTCTCCCCAGACTCTCCCACCCGTAGACG      16826
Qy    201  GTGGCGCGGAAGTGGAAGAGTGTGCGGGAACCAAGGACTGCTATGTTGTTCTATGATGTGCCT   260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16825  GTGGCGCGGAAGTGGAAGAGTGTGCGGGAACCAAGGACTGCTGGTTAGTTCTATGATGTGCCT  16766
Qy    261  GAAGAAACAGGACCTGTACAACAAGTTCAAAGGGACGGCGGTTTCTCCCACCTC           320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16765  GAAGAAACAGGACCTGTACAACAAGTTCAAAGGGACGGCGGTTTCTCCCAGCTC          16706
Qy    321  CAAGTCCCCCTGGGTGGAGTCCGAATACCTTGGATTACCTTTTTTGA                365
            |||||||||||||||||||||||||||||||||||||||||||||||
Db  16705  CAAGTCCCCCTGGGTGGAGTCCGAATACCTTGGATTACCTTTTTTGAAGTAGGTTCTGTGGG   16646
Qy    366  ------------------------------------------------------------    365
Db  16645  TAAGGGACTGAGTGGGAAGGCTGTCCATCCCATCGGGGGAGCGTGCTCAGTGCTCAGTGGT   16586
Qy    366  ------------------------------------------------------------    365
Db  16585  TCTGTTCTCCTGACCATCTGTCTCCCACTTCCCAAAGCAGAGAGGGGCAGCCTCCCTCGGGCCA   16526
Qy    366  ------------------------------------------------------------    365
Db  16525  GGCCCTTTGAGATGGGGTGTGGGGGACCAGCAACAGCAGAGGGACCATGTCTGGCGAGCCTGTC   16466
Qy    366  ------------------------------------------------------------    365
Db  16465  AGGGAGTTAGGGGGAGCTCCAGCCAGCAATCTCACCGTGCACCCTCTGCTAACAAT        16406
Qy    366  ------------------------------------------------------------    365
Db  16405  GTTCATTATTTTCAGTTGAGCACCATTTTGGTCATGGACTACACAAGGCACTTTATATGC    16346
Qy    366  ------------------------------------------------------------    365
Db  16345  TTATTCCTATTTTTTTATGTTCAGCTTCTCTCTCTTAAAAACAAATGTTTAAAACCAATTCTG   16286
Qy    366  ------------------------------------------------------------    365
Db  16285  GGCCAGGCGTGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCAGGTGGA    16226
Qy    366  ------------------------------------------------------------    365
Db  16225  TCACCTGAGGTCAGGAGTTTGAGACCACCCTGGCCAACATGGCAAAACCCGTCTCTTTACT   16166
```

```
Qy    366 ------------------------------------------------------------ 365
Db  16165 AAAAATACAAAAATTAGCCAGGCGTTGGTGGCAGGCACCTGTAATCCCAGCTACTCGGGAG 16106
Qy    366 ------------------------------------------------------------ 365
Db  16105 GCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGCGGAGGTTGCAGTGAGCCGAGATCACG 16046
Qy    366 ------------------------------------------------------------ 365
Db  16045 CCCCTGCACTCCAGCCTGGGCGACAGAGCGTCTCAAAAGAAAAAAAATTAATAAACAAGA 15986
Qy    366 ------------------------------------------------------------ 365
Db  15985 AAAAAAAACAAATTCTGTTTGCAAAAGTATTTCTATACACTGTAGAAATTTGTGGGGGG 15926
Qy    366 ------------------------------------------------------------ 365
Db  15925 TGGGGGGGGTAAAGATGATAGAAAAAAAAAATGTCCCATGCTTACTGGCAGAAATCATGTAT 15866
Qy    366 ------------------------------------------------------------ 365
Db  15865 TGACATTGGGTGAGGAGGGCACTTTTTTTTTTTCAGTCTATTTTTAATCTTCACAGCAAA 15806
Qy    366 ------------------------------------------------------------ 365
Db  15805 CTTGTGAGGTTCATTCCATCAACCTGAGACTCACAGAAGCTAAGAAACTTGATACCGGCT 15746
Qy    366 ------------------------------------------------------------ 365
Db  15745 AGTAACCAGTGGACTTGATACCGGCTAGTAACCGGTGGACATAGAGTGAACTGGATCTTT 15686
Qy    366 ------------------------------------------------------------ 365
Db  15685 CTGACCTCGGGCGAGGGCGCGGGGTAACAAAGGGAGGGATAAATGCCCAGACAGTGTCCTCAGA 15626
Qy    366 ------------------------------------------------------------ 365
Db  15625 GAGCTGAGAGCTGTAACTTGCTGCCCGGGCCTTCTCACAGTGTTCAAGGACAAAAATAAGGC 15566
Qy    366 ------------------------------------------------------------ 365
Db  15565 TTTAAGAGAGAAGAGGGACAGAGACTGATTGCACGGGCAGAGACATGGTTAGAGAAAGGA 15506
Qy    366 ------------------------------------------------------------ 365
Db  15505 AGAAGAGATGATTCGTGTGGGAAAGAAGAACTGGCTCGGTGGATGGGATAGAAAGAAGGGGAAGGA 15446
Qy    366 ------------------------------------------------------------ 365
Db  15445 CAGATGGGTAAGAAGAAAAGGGAGGAGGGATGGAGGGGATGGAAGCAATGGAAAAAATGG 15386
Qy    366 ------------------------------------------------------------ 365
Db  15385 GAAGGAAGGAGGTTGGATGGAAGGATAGAATGCCTATTAGCAAAAAAAATARGTGTGGATAG 15326
Qy    366 ------------------------------------------------------------ 365
Db  15325 AGAGATGGAGGATAGGAAGTAGTTAGTCAAGGTTCTCCAGAGAAAACTGAACCAATAGGA 15266
Qy    366 ------------------------------------------------------------ 365
Db  15265 TATATACAGATACACTAAGAGAGGAGGCCAGCGGCGTGGGCTCAAGCTTGTAATCCCA 15206
Qy    366 ------------------------------------------------------------ 365
Db  15205 GCACTTTAGGAGGCCGGGATCACGAGGTCAGGAGATCAAGAGACCATCCTGGGCT 15146
Qy    366 ------------------------------------------------------------ 365
Db  15145 AACACAGTGAAACCCGACTCTACTAAAAATACAAAAAAAATTAGTTGGGCGTGAATGAT 15086
Qy    366 ------------------------------------------------------------ 365


Db  15085 GTGCGCCCTGTAGTCCCAGCTGCTCGGGGAGGCTGAGGCAGGAGGAATGGCGTGAACCCAGGA 15026
Qy    366 ------------------------------------------------------------ 365
Db  15025 GGCGAGAGCTTGCAGTGAGCTGAGATCGTGCCACTGCACTTCAGCCTGGGTGACAGAGCAA 14966
Qy    366 ------------------------------------------------------------ 365
Db  14965 GACTCCGGTCTCAAAATAAATAAATAATAAATAAAAGAGGCCATGGTGGCTCACA 14906
Qy    366 ------------------------------------------------------------ 365
Db  14905 CCTGTAATCTGAGCACTTTGGGAGGCCGAGGCGGGCGGATCATTTGAGATCAGGAGAGTTCA 14846
Qy    366 ------------------------------------------------------------ 365
Db  14845 AGACCAGCCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAAGTTACCGT 14786
Qy    366 ------------------------------------------------------------ 365
Db  14785 GTGTGGTTGGCACACACCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATTGCTT 14726
Qy    366 ------------------------------------------------------------ 365
Db  14725 GAACTTGGGAGGCAGGAGGTTGCAGTGAGCCGAGATCACGACCACTGCACTCCAGCCTGGGT 14666
Qy    366 ------------------------------------------------------------ 365
Db  14665 GACAGAGCAAGACTTTGTCTCAAAAAAAAAAAATTTATAATAAGAGGAGATTTATTATGG 14606
Qy    366 ------------------------------------------------------------ 365
Db  14605 GAATTGGCTCATGCGAATCACAGACACAAAAATGTCCCCAGCATGCAGTGCATCATGGGCTGGA 14546
Qy    366 ------------------------------------------------------------ 365
Db  14545 CAACCAGGAAAGCTTGTTGGTGTGGGTGTTGATTCGTGTCTGAGTCTGAAGGGCCAAGGCCCAGGGGAGC 14486
Qy    366 ------------------------------------------------------------ 365
Db  14485 AGTGGGTGTTACCCCCCAGTCGGAGGGCCACAGCCAATCAGAGAGGGGGCCCACTGATATAA 14426
Qy    366 ------------------------------------------------------------ 365
Db  14425 GTCCCAGAGTCCAAATGCCGGGAGAACAGGAAGCTCCAACGTCCTAAGGACCAGGAGAAGTTG 14366
Qy    366 ------------------------------------------------------------ 365
Db  14365 ATGTGCCAGTCAGGAAGAGAGAATGGAATGGCATTCCTCCTCCATTTTTGTTCTC 14306
Qy    366 ------------------------------------------------------------ 365
Db  14305 TTTGGGCCGTCAGTGGATTGGATGATGCCCGCACACTGGGTGAGGACAGAATCATCACCA 14246
Qy    366 ------------------------------------------------------------ 365
Db  14245 AATCTGCCGATTAAAAATGTTAATCTCTTCTGGGAAAATCCTCACAGATGGGCCCAGAAT 14186
Qy    366 ------------------------------------------------------------ 365
Db  14185 AAATGTTTTACTGTCTACCTGGGTATCCCTTAGTGCAGCTAAATTGACACATAAACTTAAC 14126
Qy    366 ------------------------------------------------------------ 365
Db  14125 CATCACAGGCGCAGGCACTGGCTCACACCTGTAATCCCATCACTTTGGGAGGCCGAGGT 14066
Qy    366 ------------------------------------------------------------ 365
Db  14065 GGGAAGGATCCTTTGAGGATGAGGGTAGGAGGCAGATCACTTGAGCCCTAGGAGTTCAAGACCAGC 14006
Qy    366 ------------------------------------------------------------ 365
```

```
Db  14005  CTAGCCAACATAGGGAGAGACCTCGTCTCTACAAAAAAAAAAAAAAATTAAATTCGCTGGGT  13946
Qy    366  ------------------------------------------------------------    365

Db  13945  ACGGTGGTGGGCACCTGGTCCCAGCTACTCTGGGAGGCCAAGGTAGGAGGATCGAACTTGA  13886
Qy    366  ------------------------------------------------------------    365

Db  13885  GCCCAGGAGGTCAAGGCTGCAGTGAGCCATGAGTTCCAGCCTCGGTGA              13826
Qy    366  ------------------------------------------------------------    365

Db  13825  CAGAGCAACACCCTGTCTTAAAGAAAAGAAAAATTTAACCATCACAGAAGGCAGAGAAGAAA  13766
Qy    366  ------------------------------------------------------------    365

Db  13765  AGGCAGAATGGGGTGGATGAGGTGGGTGAGTAGTATGTATAGGAAGGGACGATCCAG       13706
Qy    366  ------------------------------------------------------------    365

Db  13705  GCAGGGAAGGAAGGGCTGGAGCGAAGGAGAAGCAAGGAGGAAGGAGAGACAGAA         13646
Qy    366  ------------------------------------------------------------    365

Db  13645  GGAAGGAGTGTGTAGAAAGGTGAAAGAGAAAAAGAGAAGAATGGATTGTATGGGGAAGAAATGGATG  13586
Qy    366  ------------------------------------------------------------    365

Db  13585  AGTAGGTTAGAAGGCTCACTCGGCTAGATAAAAGGTGAGAAGTATAAATGAATAATAAGAA  13526
Qy    366  ------------------------------------------------------------    365

Db  13525  AGGAGGCATAGGAAGACAGGAAGGCTCTCGGCTAGAAGAATGGCAGACAAACCACAATAAT  13466
Qy    366  ------------------------------------------------------------    365

Db  13465  GGGAGGAGGAAGGAAGGAAGGATGGATGGATGGCTGGAAGGAAAGGGAAG             13406
Qy    366  ------------------------------------------------------------    365

Db  13405  GATAAGAAGGACAGACAGGAAGGCTCTCGGCTAGAAGAATGGCAGACAAACCACAATAAT   13346
Qy    366  ------------------------------------------------------------    365

Db  13345  TGCTGAAATGGGGTAGGAATAAGACATTAGAGAAGAAATAAAAGGGAAAGAGAACACAAAGATATTTAA  13286
Qy    366  ----.-------------------------------------------------------    365

Db  13285  AATGTTTTCATTAATTTTTTGCCTCCTCCCTGAATTCTTCCTGATTCTTCAGCCCACAT    13226
Qy    366  ------------------------------------------------------------    365

Db  13225  CCCAAGCCAGGGTGATCCTTCCTGCCTTTACACTCCCCTCCACACTTTTTGTCTCTCATA   13166
Qy    366  ------------------------------------------------------------    365

Db  13165  TGTGGCCGGTGGTCACTTTCTTTGGTAGTTGCATATTTCATTTACCCAAACTTCAGC      13106
Qy    366  ------------------------------------------------------------    365

Db  13105  TCCTGAAGGTCAGGATACAAGGAGGCCTCATCTCCGCATTCCCTCCCTTCCTGA         13046
Qy    366  ------------------------------------------------------------    365

Db  13045  AGCTTGAATACCTAGTCAGTACCCAGTGGATGTTTCCTAAACATGTAAGTAATGACATCAT  12986
Qy    366  ------------------------------------------------------------    365

Db  12985  GAAGAAGCCACACATGTTTACCTTGACCACAAACACAGGGCAAAGGTGACTAGTGTGGTCAG  12926
Qy    366  ------------------------------------------------------------    365

Db  12925  AGATCCCTGCTGCTTGGTGGGGAATCAGGGAAGGCTGCATGGGAAGAAGTGGCATTTTAGTTGAGA  12866


Qy    366  ------                                                          365
Db  12865  ACTTGAAAGGTGGTGTATATTTAGTTTTTCTTGGCTGCCTATATTCCTTGTTGTCACATTGCCCTC  12806

Qy    366  ------                                                          365
Db  12805  TCCATCTTCAAGCCACTGGGCAAGGCTAGAAGGCCCTCAACAGACTATCGGTAGGAATGT   12746

Qy    366  ------                                                          365
Db  12745  GGAAGTTGAAGACTCAGAGTGCAGAAAGAAACAAGTAGCATTTAGAGAAAGCTAAATC     12686

Qy    366  ------                                                          365
Db  12685  CCCTCCAAGAATACCTCAATCATCGTGAAAAAGCCTGTTAGTAGTAGACGCACTAACACTCAAG  12626

Qy    366  ------                                                          365
Db  12625  GCACTGCTTCACAAGGTAAGGAACGTGTAATTGAAAACTTGAGAAGGAAAGGAAGAAAACTTGTT  12566

Qy    366  ------                                                          365
Db  12565  CTGTACTGGCGAGAAAGCTTAGCAGAATTGTGTCCTGCAGTCATATGGGACACAGAGACTTG  12506

Qy    366  ------                                                          365
Db  12505  TAAATGATGAATTTGAATGCTTATCCGAGAAGGTTTCCAAATAAAATGTGGAAGGCACGG   12446

Qy    366  ------                                                          365
Db  12445  CCTGGTTTCTTCCTGCCTCTTATAGTAAAAATGCAAGAGGAGAGAGAAAATGAGGGAAG    12386

Qy    366  ------                                                          365
Db  12385  AACTTAAACAGAAAAGGAACCAGGACACTTGATGATTTGGGAGGTTCTCAACCTATGCAAAAA  12326

Qy    366  ------                                                          365
Db  12325  ACAATAAAAATTAAGAGATTGTAGCTGGGCACAGTGGCTCATGCCTGTAATCCCAGCACTT  12266

Qy    366  ------                                                          365
Db  12265  TGAGAGTCCGAGGCGAGCAGATCACTTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAATG   12206

Qy    366  ------                                                          365
Db  12205  TGGGGAAACTCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCGTGGTGGCGGGCGCACCT  12146

Qy    366  ------                                                          365
Db  12145  GTAATCCCAGCTACTCAGGAGGCTGAGGTGGGAGGATCACTTGAACCCAAGAGGCGGAGG   12086

Qy    366  ------                                                          365
Db  12085  TTGCAGTGAGCCAAGATCATGCCACTGCACTCCAGCCTGGGTGACAGAGCAAGACT       12026

Qy    366  ------                                                          365
Db  12025  CCATCTCAAAAAAAAAAAAAAGAGATTGCTCCCAAAAGTGTGACTAGAGAAACAGC       11966

Qy    366  ------                                                          365
Db  11965  CAAGTATGTGATTATACCAAACTTCAGGAAGATAAAAGATACTCAGTCGCTCAA         11906

Qy    366  ------                                                          365
Db  11905  AAGGCTCTTTGAAGAGATTAAGATTATAACTCACAGTCCCCTTCAATCAAAACCAGGGGGAC  11846

Qy    366  ------                                                          365
Db  11845  TTCTAGGAAGCTGAACAGCACATTGTCCCTCAGCCATCTCAGCTGCGGAGCCAAAGTAGAGAA  11786
```

```
Qy     366 -------------------------------------------------------------- 365
Db   11785 GGGCTTATCTTGAAAAAAGGATCTGTCCTTGGCTTTTATCTAATAATGCAGTGGATTCC 11726

Qy     366 -------------------------------------------------------------- 365
Db   11725 CCCATGACATCCATAGGAGACCCGTAAAGTTCCTGAGACGTTTACATCCACAGAAACACT 11666

Qy     366 -------------------------------------------------------------- 365
Db   11665 GTTAGCTTGGATTAAATGGAACACAGAGAGTATGAAATCAAAGAAGAGGCTTGGACTCTC 11606

Qy     366 -------------------------------------------------------------- 365
Db   11605 CAGTTTCTTACTGTTGGAGATGCAGACTGGTAAAACTTAGCTGCAAACACCTGCTTACCT 11546

Qy     366 -------------------------------------------------------------- 365
Db   11545 TTAGTGAAAAGGAGGAATATCTCAGACGGTGAAACCAGAGAAGCTCAGTAGTGCTAAG 11486

Qy     366 -------------------------------------------------------------- 365
Db   11485 AGCGAAAGAGAATTCTTCCCAGGCCCTGAAACCTAATGGAGTTTTCTTCTGGCTGGATTTTTC 11426

Qy     366 -------------------------------------------------------------- 365
Db   11425 AAAACTGCATTGGACCTGATTGTGTCCCTTTCATGTCCCCATGCCTTGAGCCAGATTG 11366

Qy     366 -------------------------------------------------------------- 365
Db   11365 TCTGCAACTGTTATCCTGTGTCCCCACATTTTATGTTGGGAGCGAGAAAACTTTAGTT 11306

Qy     366 -------------------------------------------------------------- 365
Db   11305 TTGCTGGCCCACAGATAGAGAGAAACTGTACCCCGAGAGTTGTACTGACTGGACTATGCC 11246

Qy     366 -------------------------------------------------------------- 365
Db   11245 CAGAGTCTATTTGACTCTGACTTAGATACTGTTGAGTTGGGAATTGAGTTGATGCTGTA 11186

Qy     366 -------------------------------------------------------------- 365
Db   11185 ATGAGAATGAGACATTTGGGGGGACATTGGGAGTGATGAAATTTTGCATTTGAAAGAGA 11126

Qy     366 -------------------------------------------------------------- 365
Db   11125 TGTGGGGTTGGGGTAATCCAGCCCACACTGTAATCCCAGCACACTTTGGGAGGCCGAGGCAG 11066

Qy     366 -------------------------------------------------------------- 365
Db   11065 GCAGAATCACCTGAGGTCGCGGCAGTTCGAGACCAGCCTGACCAACACCCATCT 11006

Qy     366 -------------------------------------------------------------- 365
Db   11005 CTACTAAAAATACAAAAATTAGCCAAGCATGGTAGCACATGCCTATAATCCCAGCTACTCG 10946

Qy     366 -------------------------------------------------------------- 365
Db   10945 GGAGGCTGAGGCAGTAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCGGTGAGCCGAGAT 10886

Qy     366 -------------------------------------------------------------- 365
Db   10885 CACGCCATTGCACTCCAGCCTGGGCAACAAGAGTGAAACTCCATCTAAAAAAAAAGAA 10826

Qy     366 -------------------------------------------------------------- 365
Db   10825 AAAAGAAGAGAGTGGATTTTGGGTGGGGGAGACAAGGTAGGCAGAATG 10766

Qy     366 -------------------------------------------------------------- 365
Db   10765 ATCCTCTAAAGTGCTCTGCCCTTAATCCCAGAAGCTTAAGAATATGTTAGATGTCAGTAT 10706
```

```
Db   10705 TGCGTGGGCAGTAGGAATCTTAATTAACGTTATAGACTGTTTATGGTTTGAAATGTCCCCTCT 10646

Qy     366 -------------------------------------------------------------- 365
Db   10645 AAAACTCCTGTTGACATTTAATCATCATTGTTGATTGCATTAAGAAGTGGCCCTGTTAAAA 10586

Qy     366 -------------------------------------------------------------- 365
Db   10585 GGTGATTTAGTCCTTAAGAAACGCTGCCCCATGAATAGATCAGTCTTGCGGGAG 10526

Qy     366 -------------------------------------------------------------- 365
Db   10525 TGTGTTTATCAAGAAGTGTTAAAAAGTGAGTTCTGGCCAGGGGCAGGTGGCTTATGC 10466

Qy     366 -------------------------------------------------------------- 365
Db   10465 CACTCAGCACTTTGCGGGGCCAAGACTTGAAGTGCAGTTGTTTGAGACCCTGGCCAAC 10406

Qy     366 -------------------------------------------------------------- 365
Db   10405 ATGGTGAAAGTCTGTCTCTACTAAAAATACAAAAAGTGTCCGGGAGTGGTGGCGCGCGC 10346

Qy     366 -------------------------------------------------------------- 365
Db   10345 CTGTAATCCCAGCTGTCCAGGAGGCCGAAGCAGCAGGAGGATCGGCATGAATCCCGGAGGCAGA 10286

Qy     366 -------------------------------------------------------------- 365
Db   10285 GGTTGCAGTGAGCTGAGATCGCCCCGTTGCACTCCAGCCTGGGTGATAGAGCAAGACTCT 10226

Qy     366 -------------------------------------------------------------- 365
Db   10225 GTCTCAAAAAAAAAAAAAAAGAGAAAAGAGAAAGAAAAGAGAAAGAAAGAGAAAAAGA 10166

Qy     366 -------------------------------------------------------------- 365
Db   10165 AAGAAAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGAAAGAAAGAAAGAAAGAAA 10106

Qy     366 -------------------------------------------------------------- 365
Db   10105 GAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAGAAAGAAA 10046

Qy     366 -------------------------------------------------------------- 365
Db   10045 AAAGAAAGAAAGAAAAAAAGAAAAAGAAAAAGAAAGAAAGAAAGAAAGAAAG 9986

Qy     366 -------------------------------------------------------------- 365
Db    9985 AAAGAAAGAAAAGAAAAGAAAAGAAAAAGAAAAGAAAGAGTAGGTCTGCCC 9926

Qy     366 -------------------------------------------------------------- 365
Db    9925 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 9866

Qy     366 -------------------------------------------------------------- 365
Db    9865 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCTTACTCTCACCCTCTCTTG 9806

Qy     366 -------------------------------------------------------------- 365
Db    9805 CCCTTCCACTTGCCACCATGGGATGAAGAGAGGGAGAAAGGCCCTCACCAGATGCCAGTGCCA 9746

Qy     366 -------------------------------------------------------------- 365
Db    9745 TGCTCTTGGGACTTCCAAGTCTCCCAGAAAACATGAGCCAAATACACTTCTGTTCATTTATAAA 9686

Qy     366 -------------------------------------------------------------- 365
Db    9685 TTACCCAGCCTGTGATATTCTGTAATAACAACACAAAATAGACTGAGACAATAGATCTTCA 9626
```

```
Db  9625 AATAGTGAGGTTATCCTGGTAATCCAGATGGGGGCCCAATCTAATCCCATGAGCCTTTAAA 9566
Qy   366 ------------------------------------------------------------  365

Db  9565 ACTTTCTCCAGATGGATGGAGGCAGAAGAGAGAAGGGGAAGTCAGAGAGATTTGAAG 9506
Qy   366 ------------------------------------------------------------  365

Db  9505 CATAAACAGGACTCCATGGTGCCGTTTCTCGGTTGACGATGGAGGTGGGTAACGTGATGAAA 9446
Qy   366 ------------------------------------------------------------  365

Db  9445 AATGTGGGGTGCCTTCCGGGAGGCTCCCACTAACACATCGGACAAACAGGGGAC 9386
Qy   366 ------------------------------------------------------------  365

Db  9385 CACAGCCCTACAGCCACAAAGAACCTAAGTTTTGCTGACAACCCAGGGGGGCTTGGAAGTG 9326
Qy   366 ------------------------------------------------------------  365

Db  9325 TCTTCTCCCCCATCGGTTCCAGATGTGAGACCCAGAGCGGAGGAACCAGCTGACCCCACC 9266
Qy   366 ------------------------------------------------------------  365

Db  9265 TGGTGTGGTAATTGTTATGACAGCAAATAGAAAAGAATCCAGATGGGGCAGGATCTGCCAG 9206
Qy   366 ------------------------------------------------------------  365

Db  9205 TGTGTGGTAATTGTTATGACAGCAAATAGAAAAGATAATAAGTTTGTATCATTTTTAAGGCACTGTG 9146
Qy   366 ------------------------------------------------------------  365

Db  9145 GCCAGTGACATGTGGAGGGCACCCAGGGCGGATGGGAGGGGCACGCAGGGTCAGC 9086
Qy   366 ------------------------------------------------------------  365

Db  9085 AATGAGCTTGCCCAGGTCACCTCTCCTCTCTAAGCCTCAGTTTTCCTCTCTATGAAATGA 9026
Qy   366 ------------------------------------------------------------  365

Db  9025 GAGTAGTGATATCTCCCTCCCAGGGTCAGTGCAAGGCTCAAAATAACACAGATTATTAAGGTGC 8966
Qy   366 ------------------------------------------------------------  365

Db  8965 TAGGTGCACAAGAAGTGTTTGAAACATGCCTAGTGTGCTTTCCATTCCAAGAGAGCTCTC 8906
Qy   366 ------------------------------------------------------------  365

Db  8905 TGGGTCTTGGGGGATGGGAGGGCAGTGGCGCCCCTCGGGGATTACTGACAGTCCTGCTCTGTT 8846
Qy   366 ------------------------------------------------------------  365

Db      ------AGTTGGAGCCGCGCCCCCACCCTGTCCTGGTGCTCACCCGACGGAGGAGAGATCCTGAGT 8786
Qy   366 ------------------------------------------------------------  365

Db  8845 TCTGCGAGTGGAGCCGGGCGCCCCACCTGTCTCCCTGGGTGTCACCCGACGGAGGAGAGATCCTGAGT 8786
Qy   421 GCCAATGCCACGTACCAGTTGCCCCCTCCCATGCCCCACACTGTTTTCTGAAGTATGAGGTG 480

Db  8785 GCCAATGCCACGTACCAGCTGCCCCCCACTGTTTTCTGAAGTATGAGGTG 8726
Qy   481 GCATTTTGGGGGGGGGGGGGGGGGCGGGAACCA 508

Db  8725 GCATTTTGGGGGGGGGGGGGGGGGAACCAAGGTGGGGAAGCTCCTTTTCCTGCCCCAGGCTA 8666
Qy   509 ------------------------------------------------------------  508

Db  8665 GGCCGGCTCCTCCACCCCTTCTTACTCAGGTTCTTCTCACCCTCCCAGCCTGCTCCCTGCA 8606
Qy   509 ------------------------------------------------------------  508

Db  8605 CCCCTCCTCCAGGAAGTCTTCCCGTACACTCCTGACTTCTGGCAGTCAGCCCTAATAAA 8546
Qy   509 ------------------------------------------------------------  508

Db  8545 ATCTGATCAAAGTATGATGACCTACAGGAGGAGGCCTGCTTGCCAAGTCAACAGATTCAGTAC 8486
```

```
Qy   509 ------------------------------------------------------------  508
Db  8485 AGAAAAAACTGAAAAAATACAGATAAGCTTAAGAAGCAGAGACCAAAAAGTACCAGAGATGAC 8426

Qy   509 ------------------------------------------------------------  508
Db  8425 CACACATCACTCTGGGTGTATATCCAATTCAGATTTGTTTTCTGTGTATGCATGTGTGTA 8366

Qy   509 ------------------------------------------------------------  508
Db  8365 TAGCTGCATTTATTTATTGGCAAGGGCTGGCAGACTTTCCCGGAAGAAGGCCAGATAGTCGA 8306

Qy   509 ------------------------------------------------------------  508
Db  8305 TATGTTTGGCTTCATGGGGCCGTATGTTCGCTCAGGACTACTCAACGCTGCAGTTATAGCA 8246

Qy   509 ------------------------------------------------------------  508
Db  8245 CAAAAGGAGCCGTAGCCTATACGTAAATGAATGGGCATCGCTGGGTTCAGTAAAACTGT 8186

Qy   509 ------------------------------------------------------------  508
Db  8185 TTACAGGGCCAGGTGCGGTGGCTCATGCCTGTAATCTCAGTACTTTGGGAGGCCGAGGTGG 8126

Qy   509 ------------------------------------------------------------  508
Db  8125 TGGGAGGATTACCTTAGCCCAGGAGTTCAAGACCAGCCTGGGCAACATGGTGAAACATTA 8066

Qy   509 ------------------------------------------------------------  508
Db  8065 TCCCTACAAAAATAAAAAAAAAAAGCTGGGCGTGGTGGTGCATGCTTGTGGTCCCAGCTGCTTG 8006

Qy   509 ------------------------------------------------------------  508
Db  8005 GGATGCTGAGGCAGGAGGAGGATCGGCTCGAGCCCAGGAGGCCACAGTGAGCCATGATC 7946

Qy   509 ------------------------------------------------------------  508
Db  7945 GCACCACTGCACTTTAGTCTGGGCAACAGAGTGAGACCTTGTCTCAAAAAAACAAAAA 7886

Qy   509 ------------------------------------------------------------  508
Db  7885 TAAAACTTTTTACATAAAACACAGAACTTGGTCCCTGGGCCTCTGCTCTTGA 7826

Qy   509 ------------------------------------------------------------  508
Db  7825 ATGTTCTTGCTTCCACTAAAGTAACATTCACACTCCGGATTTTTGCATACTCTGGGTTCT 7766

Qy   509 ------------------------------------------------------------  508
Db  7765 GGGGAATATAGATCCGAATCCAGCGTGGTTCCTGCCTTCAAGAACCTCACAAATATTCTA 7706

Qy   509 ------------------------------------------------------------  508
Db  7705 GACCAGCACTGCCCAATAGAAAGAAAATATAATGCAAGCCACACATGTGCAGTTTAAGTGTT 7646

Qy   509 ------------------------------------------------------------  508
Db  7645 CCATGTTAAATTAAGTAAAAGAGACAGGTAAATCGAATTTAATAACAGATTTTACTTC 7586

Qy   509 ------------------------------------------------------------  508
Db  7585 ATCCAATTGAATGGTATCATTTCAAATGAGCAATTCTGATAGTGATTGAGATCTTTTACAT 7526

Qy   509 ------------------------------------------------------------  508
Db  7525 TCTTTTTCACTACGTCTTTTAAAAATCTGATGTGTGTTTTTGTACTTGGAACACTTCTCAGTG 7466

Qy   509 ------------------------------------------------------------  508
Db  7465 TGGACCAGATGCATTCACATACTCAGTAGTCACGGGTGCCTTCCATACCACA 7406
```

```
Db  5245  CTAGTGGTCAGCTGCTTGATAACACCCTGCTTCCTGGCTGCTCCCCAGTCCCATCTGGT  5186
Qy   801  ------------------------------------------------------------   800

Db  5185  GTGTTCTTGGGATCATCTCCCAAAGAAACTGCTTACACTTGAGCCTTGTCTGAGGTCTGT  5126
Qy   801  ------------------------------------------------------------   800

Db  5125  TTCTAGGGGAATTCAGATGATGATAATTATGCTTCAGGAAAGCCTAAATTTTCTGCTTTT  5066
Qy   801  ------------------------------------------------------------   800

Db  5065  CTCTTCCCTTACCCAAAATCAGGACTTTTCTGGACACACACCCTGTGGCTAACCTTTCAGC  5006
Qy   801  ------------------------------------------------------------   800

Db  5005  CCAGCAGACCAGAGTCCGTGAATGACTTGTTCCTCTGTCCCCAAAAGGAAACTGACCAGAG  4946
Qy   815  ------------------------------GGAACTGACCAGAG   814

Db  4945  GGGTCAGGCCGGACGGCCCTCGAGTCAGGGCCCCACCCAGCAGCAAGACAGGAGAGAGG   4886
Qy   815  GGGTCAGGCCGGACGGCCCTCGAGTCAGGGCCCCACCCAGCAGCAAGACAGGAGAGAGG   874

Db  4885  ACCTTGCAGAGGACGAAGGAGGAGGATGAGGAGGACACAGAAGATGGGGTCCAGCGTTCC  4826
Qy   875  ACCTTGCACAGGAGGACGAAGGAGGAGGATGAGGAGGACACAGAAGATGGGGTCCAGCGTTCC   934

Db  4825  AGCCCTACAHTTGAACCACCTTCTTTCTCTGGGCAAGACCACCCAGGGCTTCCAGGGCACTCGG   4766
Qy   935  AGCCCTACAHTTGAACCACCTTCTTTCTCTGGGCAAGACCACCCAGGGCTTCCAGGGCACTCGG   994

Db  4765  AGGCTGGTGGGGGTGGGATCAGGGAGGGGGCCCAGGGCTCCTCGTGGTCCCAAGCGAAGGCTCCT  4706
Qy   995  AGGCTGGTGGGGGTGGGATCAGGGAGGGGGCCCAGGGCTCCTCGTGGTCCCAAGCGAAGGCTCCT  1054

Db  4705  CTGCTTGGGAATTCTTCAGACAGAAGCTGGGCGGGCCAGCACTGTGGACTCGGGTTTCCTCCTGGAAGAGAGCTCC  4646
Qy  1055  CTGCTTGGGATTCTTCAGACAGAAGCTGGGCGGGCCAGCACTGTGGACTCGGGTTTCCTCCTGGAAGAGAGCTCC  1114

Db  4645  AGGCTGGTGGGGTGGGACTCAGGGAGGGGGCCAGGGCCCCAGGGGCTCCTCCTGGAAGAGGAAGGCTCCT  4586
Qy  1115  CTGGGTCCTCTCTGGCTATTTGGCTGTGAGGAGGGGGGCCAGGGCCCCGGGTCGGGGGTTGGGGATGGGC  1174

Db  4585  ACCAAGAATCTCTCCCACCTGAATCTCCAAGGACTCGGGTTTCCTGGGTTTCCTGGGACAGGG  4526
Qy  1175  ACCAAGAATCTCTCCCACCTGAATCTCCAAGGACTCGGGTTTCCTGGGTTTCCTGGGACAGGG  1234

Db  4525  CAGAAGAATAACCTCTCCTCTCTCTGGGCCACCTTACCACGGGATCCGAAACCTGGGCCCAC  4466
Qy  1235  CAGAAGAATAACCTCTCCTCTCTCTGGGCCACCTTACCACGGGATCCGAAATCTGG  1294

Db  4465  TCCCTGGGGGACCCCCAGTTTCTTCAGACACTGACCTTGTCTGGGGAAAGCAGCCCTG  4406
Qy  1295  TCCCTGGGGGACCCCCAGTTTCTTCAGACACTGACCTTGTCTGGGGAAAGCAGCCCTG  1354

Db  4405  AGGAGGAAGAGAGGCGGAGGAATCAGAAATTGAGGACAGCAGCGATCTGGGGG  4346
Qy  1355  AGGAGGAAGAGAGGCGGAGGAATCAGAAATTGAGGACAGCAGCGATCTGGGGG  1414

Db  4345  CTGAGAGCACCCGGAGGACCGGGACATTGGGGCATTACATGGGCCAGGT  4286
Qy  1415  CTGAGAGCACCCGGAGGACCGGGACATTGGGGCATTACATGGGCCAGGT  1474

Db  4285  GA  4284
Qy  1475  GA  1476
```

RESULT 2

LOCUS   AL358412   173352 bp   DNA   linear   HTG 30-OCT-2000
DEFINITION Homo sapiens chromosome 1 clone RP11-509F14, *** SEQUENCING IN
            PROGRESS ***, 16 unordered pieces.
ACCESSION   AL358412

VERSION   AL358412.9 GI:11071692
KEYWORDS   HTG; HTGS_PHASE1.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 17352)
  AUTHORS   Sims,S.
  TITLE   Direct Submission
  JOURNAL   Submitted (29-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
            On Nov 1, 2000 this sequence version replaced gi:11071629.
COMMENT   -------------------- Genome Center
            Center: Sanger Centre
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------------- Project Information
            Center project name: bA509F14
            -------------------- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Consensus quality: 167382 bases at least Q40
            Consensus quality: 169011 bases at least Q30
            Consensus quality: 170100 bases at least Q20
            Insert size: 171852; sum-of-contigs
            Insert size: 189168; agarose-fp
            Quality coverage: 5.54x in Q20 bases; sum-of-contigs Quality
            coverage: 5.18x in Q20 bases; agarose-fp
            *
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 16 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *
            *   1   9825: contig of 9825 bp in length
            * 9826   9925: gap of 100 bp
            * 9926   26225: contig of 16300 bp in length
            * 26226   26325: gap of 100 bp
            * 26326   29517: contig of 3192 bp in length
            * 29518   29617: gap of 100 bp
            * 29618   35632: contig of 6015 bp in length
            * 35633   35732: gap of 100 bp
            * 35733   49745: contig of 14013 bp in length
            * 49746   49845: gap of 100 bp
            * 49846   66204: contig of 16359 bp in length
            * 66205   66304: gap of 100 bp
            * 66305   72839: contig of 6535 bp in length
            * 72840   72939: gap of 100 bp
            * 72940   83722: contig of 10783 bp in length
            * 83723   83822: gap of 100 bp
            * 83823   91894: contig of 8072 bp in length
            * 91895   91994: gap of 100 bp
            * 91995 103783: contig of 11789 bp in length
            * 103784 103883: gap of 100 bp
            * 103884 110994: contig of 7111 bp in length
            * 110995 111094: gap of 100 bp
            * 111095 127550: contig of 16456 bp in length
            * 127551 127650: gap of 100 bp
            * 127651 137959: contig of 10309 bp in length
            * 137960 138059: gap of 100 bp
            * 138060 151496: contig of 13437 bp in length
            * 151497 151596: gap of 100 bp
            * 151597 154539: contig of 2943 bp in length
            * 154540 154639: gap of 100 bp
            * 154640 173352: contig of 18713 bp in length
FEATURES   Location/Qualifiers
     source   1..173352